Scoring table: Sequence: Title: Perfect score: US-10-001-885-31 1192 1 aaaccgcctggagcc IDENTITY_NUC
Gapop 10.0 , Gapext 1.0 aaaccgcctggagccgccgg.....gaagaggacacacggaaccc 1192

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:

6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database GenEmbl: * gb_ba:*
gb_ntg:*
gb_om:**
gb_ov:*
gb_ov:**
gb_pat:**

gb_pr: gb_ro: gb_ro: gb_sts: gb_sts: gb_sts: gb_sts: em_ba: em_on: em

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

TITLE	AUTHORS	1 01	ACCESSION VERSION	RESULT 1 AX431088 LOCUS DEFINITION		a 4.5		41	C 40	C 38	نا ديا	0 35	دا ددا	υ 2 2 2 2	30 31	29	27 28	26	2 C 4 n	22 23	c 21	19 20	ш	C 17		μн	c 12	10		0 7	on u		ωĸ	, , , ,	Result
Compositions	Recipon, H., Li	Homo sapiens NISM Homo sapiens Eukaryota; Me Mammalia; Eut	AX431088 AX431088.1 GI	AX43108 Sequenc		5.6 4.7 18	4 4.7 25	6.4 4.7 25	6.8 4.8 20	7.2 4.8 25	7.2 4.8 18:	7.4 4.8 25	7.6 4.8 11	18.4 4.9	.8 5.1	2.2 5.2	л 64 44 л л 44 и	v. v.	75 6.3	5.4 6.3 17 5.4 6.3 18	88.2 7.4 23	.8 19.5 19.5	36.4 19.8 138	50.6 21.0 21	294 24.7 240	306 25.7 27	75.4 31.5	.8 32.9	32.8 36.3	473 39.7	473 39:7	8.8 67.9 165	84.9	1192 100.0	% Query Score Match Lengt
and methods relating to ov	.u,C., Salceda,S., Sun,Y.,	(human) tazoa; Chordata; Craniata; heria; Primates; Catarrhini	:21656065	1192 bp DNA om Patent W00240535.	ALIGNMENTS	3 AC11717	u w	3 AEU1483 10 RRHYDS	2 AC14651	3 AE01483	3 AC11707	3 AC11707	2 PFMAL6	6 AX43107	1545 6 AX535007 1623 6 AX497809	6 AX64431	6 AX43108	6 AX64427	6 AX64436	10 ACIZIE	2 AC094926	6 AR42570	2 AC10978	2 AC12741	2 AC11167	2 AC11623	11 G22561	თ თ	, o	ש מ	0 1	ာ ဖ	o v	9	th DB ID
ovary specific genes and	Cafferkey,R. and	Vertebrata; Euteleostomi; i; Hominidae; Homo.		linear PAT 28-JUN-2002		17176 Dictyost	Dictyos Dictyos	3410	4651	AEU14836 Flasmodiu AX431086 Sequence	707	AC117075 Dictyoste	100	107	AX497809 Sequence	131	3108 3114	AX644276 Sequence	4436 4503	590988 Mouse	094926 Rattu	1258	9783 Mus mus	7417 Mus mu	AC111675 Rattus no	Rattu	561 human STS	0980 EST and e	1087	អ្នក	13227 Sequence	Huma	BD191093 186 human	X431088 Sequenc	Description

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Patent: WO 0240535-A 31 23-MAY-2002;
DIADEXUS INC (US)
Location/Qualifiers
            CAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACGTCTCCCTCTGCCTA
                                                                     TCAGAGCAAGAAAGCGATGCCCTTCCCAATTCTCTCAATCCTTTTATGCCGAGAAGATCT
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RESULT 2 BC013587	
LOCUS DEFINITION	1129 bp iens chromosome 10 open re
ACCESSION	MGC:9596 IMAGE:3896656), complete cas. BC013587
VERSION	BC013587.1 GI:15488919
KEYWORDS	•
SOURCE ORGANISM	Homo sapiens (human) Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates: Catarrhini; Hominidae; Homo.
REFERENCE	1 to 1129)

AUTHORS TITLE RS Strausberg, L. Feingold, E.A., Grouse, L.H., Derge, J.G.,
RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
RIschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Boldow, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Kodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schmerth, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932

JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL

Direct Submission
Submitted (04-SEP-2001) National Institutes of Health, Mammalian Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Room 11A03, Bethesda, MD 20892-2590, NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC (bases 1 to 1129)

CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, http://www-shgc.stanford.edu CA 94305

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FEATURES
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 216871: Location/Qualifiers
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Dickson,
R. M.
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., Schmutz, J., Grimwood, J., Rodriquez,
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CE 1 (bases 1 to 1049)

RES Ruben, S.M., Rosen, C.A., Fischer, C.L., N.J., Feng, P., Young, P.E., Bednarik, D.P., Endress, G.A., Yu, G.L., N.J., Feng, P., Young, P.E., Greene, J.M., Ferrie, A.M., Duan, R., Hu, J.S., Florence, K.A., Olsen, H.S., Ebner, R., Brewer, L.A., Moore, P.A., Shi, Y., Lafleur, D.W., Li, Y., Zeng, Z. and Kyaw, H.

186 human secreted proteins and Patent: JP 2002510192-A 57 02-APR-2002;

HUMAN GENOME SCIENCES INC PN JP 2002510192-A/57

PD 02-APR-2002

PN JP 2002510192-A/57

PD 02-APR-1997 US 60/040162,07-MAR-1997 US 60/04033 PR 07-MAR-1997 US 60/040626,07-MAR-1997 US 60/040161 PR 07-MAR-1997 US 60/04036,07-MAR-1997 US 60/04034 PR 07-MAR-1997 US 60/04036,07-MAR-1997 US 60/04035 PR 11-APR-1997 US 60/040536,07-MAR-1997 US 60/040163 PR 11-APR-1997 US 60/040586 PI STEVEN M RUBEN, CRAIG A ROSEN, CARRIE L FISCHER, DANIEL R SOPPET, PI KRNNETH C CARTER, DANIEL P BEDNARIK, GREGORY A ENDRESS, GUO LIANG PI YU, JIAN NI, PI PING FENG, PAUL E YOUNG, JOHN M GREENE, ANN
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1 (bases 1 to 165110)
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Human DNA sequence from clone RP11-343J3 on chromosome
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Direct Submission
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                                          AAAAAAAAAAAA 1077
                                                                                                        GACGTCTCCTCTGCCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGA
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PRI 12-JUL-2001 >me 10, complete

Submitted (12-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk On Jul 8, 2001 this sequence version replaced gi:14575291.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Repli-243J3 is from the library RFCI-11.2 constructed by the group of pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm

VECTOR: DBACG3.6

This sequence is the entire insert of clone RP11-343J3 The true right end of clone RP11-242G20 is at 139955 in this sequence. The true right end of clone RP11-242G20 is at 5588 in this sequence.

Location/Qualifiers
1. .165110

		repeat_region
	/note="AluJb repeat: matches 1306 of consensus"	repeat_region
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	<pre>/note="MLT1F repeat: matches 188541 of consensus" 2146321618</pre>	repeat region
	/note="MLTIJ repeat: matches 162 of consensus" 2088921263	repeat_region
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	/note="MIR repeat: matches 60140 of consensus" 16928. 16993	at re
	<pre>/note="MIR repeat: matches 3213 of consensus" 1662616705</pre>	repeat region
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	1160011639 /note="20 copies 2 mer tc 95% conserved"	repeat_region
	/note="Alusx repeat: matches 1294 of consensus"	7000
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	<pre>/note="MIR repeat: matches 25184 of consensus" 1035310481</pre>	H 1
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	mic DNA :9606" "	
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                                                                                     50980. .51291
/note="Alusx repeat: matches 1. .312 of consensus"
/52222. .52519
/note="Alusx repeat: matches 1. .300 of consensus"
      /note="FAM repeat: matches 2. .167 of consensus" 54433. .54629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L2 repeat: matches 2453. .2629 of consensus" 22896. .23174 /note="MLTIJ repeat: matches 117. .413 of consensus" 23215. .23346 /note="MIR repeat: matches 48. .188 of consensus" 23388. .23532
                                                                                                                                                                                                                          note="23 copies 2 mer gt 97% conserved"
                                     note="LIM4 repeat: matches 3865. .4055 of consensus" 4261. .54432
                                                                                                                                                                                     note="AluSq repeat: matches 1.
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4193. .44579
note="THEIC repeat: matches 1. .371 of consensus"
4600. .44956
                                                                                                                                                                                                                                                                                                                                      note="LTR16A repeat: matches 90. .445 of consensus" 5240. .45300
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note="112 repeat: matches 2569. .2730 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0050. .40189

note="MIR repeat: matches 1. .144 of consensus"
.057. .41290

note="MIR repeat: matches 8. .240 of consensus"
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note="CpG island"

rvidence=not_experimental

is51. .36604
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1653. .24850
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388. .42698
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585. .38254
cte="LiPAL5 repeat: matches 5480. .6157 of consensus"
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)453. .30918
note="CpG island"
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618. .31876
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89. .26685
te="CpG island"
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33. .23837
te="AluJb repeat: matches 1.
38. .24137
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e="Alusx repeat: matches l. .292 of consensus"
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                                                                                                                                                                                       .287 of consensus"
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                                                                                                         Conservative
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Birect Submission

Birren, B., Linton, L., Bartia, N., Bassien, V., Beda, F., Boushay, J., Boukhgalter, B., Erom, A., Burkett, G., Linder, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Bartia, N., Bassien, V., Beda, F., Bodysano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Devar, K., Diaz, J. S., Collymore, A., Cooke, P., DeArellano, K., Devar, K., Marquis, N., Meladim, J., HaRocque, K., Lamazares, R., Janders, T., Leboczky, J., Meldrim, J., Meneus, L., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Maylor, M., McKernan, K., McKernan, K., McCarthy, M., Meneus, L., Mhova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Maylor, J., Norman, C.H., O'Connor, T., Pierre, N., Pierre, N., Schauer, S., Severy, P., Sgencer, B., Submitted (24, 240G-2002) Mhitchead Institute/MIT Center for Genome part for Lamas, J., Tarell, A., Tavers, M., Trigillo, J., Tamer, A., Submitted, M., X., Wyman, D., Ye, W.J., 
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 5, 2000 this sequence version replaced gi:6984451. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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RESULT 5 AC021954/c LOCUS

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linear

HTG 24-AUG-2002

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalja; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 173341)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapies chromosome 10, clone RP11-57E12 AC021954 AC021954.3 GI:7417809 HTG; HTGS_PHASE1; HTGS

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Consensus quality; 16:190 bases at least Q00
Consensus quality; 16:995 bases at least Q00
Consensus quality; 16:995 bases at least Q00
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NOTE: This Is a 'working draft' sequence. It currently
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Edwards, J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 864 28-OCT-2003;
Location/Qualifiers
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EST and encoded human protein.
BD108780.1 GI:23203598
BD108780.1 GI:23203598
JP 2002010789-A/857.
Homo sapiens (human)
1 Homo sapiens
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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OY 1: OY 2:	Db Db Db	RESULT 8 AXII3082 LOCUS LOCUS DEFINITION ACCESSION VERSION VERSION VEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE ORIGIN	Qy 4:	Qy 3; Въ 3:	Оу 3:	Qy 2.	Qy 1:	Qy 1.
167 CGGATCTTGGCCAATGGGGAAATCGTGCAGGACGACGACCGCCGAGTGAGGACCACTACC 226	Sal Similarity 95.4%; Pred. No. 1.1e-102; Sal Similarity 95.4%; Pred. No. 1.1e-102; S19; Conservative 0; Mismatches 17; Indels 8; Gaps 5; 47 CGCGCCTGCAGACACCAGCATCTACTCAGCGTGGGTCACCTCTGTGAACATCACTGACTG	AX113082 Sequence 5 from Patent WO0127276. AX113082 AX13082.1 GI:13939514 Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 Dna sequences from breast tumor and uses thereof Patent: WO 0127276-A 5 19-APR-2001; CCRIXA CORPORATION (US) 1. 550 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /note="n = A,T,C or G"	21 GCCGGTGACCTCCATCCTGCTCCTCCTGCTCATGATGCTTGGTGTTCGTG 473	361 CAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGA 420	01 CCCCCGCAGCAGCAGGCAGGTGCCAGGCTGGGTGCTCAGTCCCCCTTCAATGACCT 360	41 TAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCCCCCAGGGGGTCCTGG 300	.81 TGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACCACTACCCAGCCACCAAGAGG 240 	121 TTCTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAA 180

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RESULT 9
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Best Local Similarity 96.1%;
Matches 519; Conservative
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Patent: WO 0240535-A 30 23-MAY-2002;
DIADEXUS INC (US)
Location/Qualifiers
1. .643
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Sequence 30 from Patent
AX431087
AX431087.1 GI:21656064
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Compositions and methods relating to ovary specific genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                             CTTTGTGTTAAGCGTGAGGCAGAGGGAGACGTTAGTCCAG-CATTTCCAAAGTGTGGGTG 720
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                                        CCTAGGGAGCAGGACITGGGCTTAGGGCAGGTGGAAAAATTTCCAGACTTTTTTAG--CA 954
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CTGTTTTTGTTTAATGGTATATT-TTTATTGGCTACTTTATTGTTTAGGACAAGTGGTA 1013
                                                                                        ATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACGTCTCCTCTG
                                                                                                                                          ATCAGAGCAAGAAAGCGATGCCCTTCCCCAATTCTCTCAATCCTTTTTATGGCCGAGAAG
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                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                            Score 432.8; DB 6;
Pred. No. 1.1e-97;
0; Mismatches 12;
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RESULT 11
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Sequence 306
AR415427
AR415427.1
 BD110980 519 bp
EST and encoded human protein.
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Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Patent: US 663963-A 3064 28-OCT-2003;
Location/Qualifiers
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Unclassified.
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                                                                                                                                                                                                                           GTCCTGGCCCCGCCAGCAGCAGGCAGGTGCCAGGCTGGGTGCTGCTCAGTCCCCCTTCA 353
                                                                                             CTGTGGAGCCGGTGACCTCCATCCTGCTCCTCCTGCTCATGATGCT 462
                                                                                                                                                               ATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATG
                                                                                                                                                                                                                                                                                                                      CAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCCCCCCAGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTTCTCCCGCCCCAATTCCCCCCAAATTTTGACAAAATGAAGAGACACACGGAACCC 1192
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/mol_type="genomic DNA"
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El (bases 1 to 519)

El (bases 1 to 519)

Est and encoded human protein

AL Est and encoded human protein

Pl P 2002010789-A 3057 15-JAN-2002;

EST and encoded human)

PN JP 2002010789-A/3057

PD 15-JAN-2002

PO 7-AUG-2000 JP 2000280989

PF 07-AUG-2000 JP 2000280989

PF 07-AUG-2999 US 60/147499

PI JEAN BAPUTIST DUMAS MILHE EDWARDS, SEVELIN JOBERT, JEAN EVE PI GIORDANO

C12N1/21, PC C12N15/09, C12N15/09, C07X14/47, C07X16/18, C12N1/15, C12N1/19, PC C12N1/21, OCCATAINS, C12P21/08, C12Q1/68, C12N15/00, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12P21/02, C12P21/03, C12Q1/68, C12N15/00, C12P21/02, C12P21/03, C12Q1/68, C12N15/00, C12P21/03, C12P
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480 human STS WI-12709, sequence G22561 G3:1342887 G22561.1 GI:1342887 STS; STS sequence; primer; se
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JP 2002010789-A/3057.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                 ATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATG
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Key
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
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h; Physically h; Physically h h h h h c; Gaps 5; GGGG-ACCACAGG 649	ATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGA	TTAAGTGGCACAAAATCAGAGCAAGAAAGCGATGCCCTTCCCAATTCTCTCAATCCTTTT	TTAAGTGGCACAAAATCAGAGCAAGAAGAGGCGTTGCCCAATTCTCTCAATCCTTTT	CCAAAGTGTGGGTGGGNCCGTTGGTTCCCCGAGATACTTTTAGGTGGTATGGGGCCTGCA	TGTGTGTTCCCCCTTTGTGTTAACCGTGAGGCAGAGGGAAATGTTAGNCCCAGCATTTC	TGTGTGTT-TCCCCTTTGTGTTAAGCGTGAGGCAGAGGGAGACGTTAGTCCAGCATTT 7	CAPATIGNAAGGAAACCTGGTGGTCCCTTGAAGGTTATGATCANAAAAGGGCCCCACAGG	31.5%; Score 375.4; DB 11; Length 480; nilarity 92.7%; Pred. No. 2.7e-83; Conservative 0; Mismatches 29; Indels 6; Gaps	/mol type="genomic DNA" /db_xref="taxon:9606" /map="431.2 cR from top of Chr10 linkage 25149 bind 2549 bind complement(130149)	Derived from dbEST (genbank Location/Qualifier 1480 /organism="Homo say	112: 1.5 mM : 50 mM :s-HCL: 10		shead Institute/MIT Center for shead Institute for Biomedical bridge Center, Cambridge MA 0 617 252 1900 617 252 1900 1: thudson@genome.wi.mit.edu	58 ed (199	Eutheria; Primates; Catarrhini; Hominidae; 1 to 480) I to 480) Institute/MIT Center for Genome Research;	ns Metazoa: Chordata: Craniata:

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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mus musculus RIKEN cDNA 2010107G23 gene, mRNA (cDNA clone MGC:28201
IMAGE:3989515), complete cds.
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                       Sequencing Center
Center code: BCM-HGSC
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                                  CCTCCTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTGACCTTGAGGG- 536
                                                                                                                                                                                                                                                                                                                                  CCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGT
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CTCATGAGGGGGGAGTGTTCAGTAGGATCGACTGGACTTGGTGGGGCACATCATG
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                                                                                                                                                                                                                                                                                                       CCTGAACCGGCAGCTGGTGAACATGGCTTCCCACAATGGCACCTTGGGAACCACGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTCTGGTGCAGCCCATCAGGGACCCCACAGCG-CCTGGGAGGATGGTGCGGATCTTGGC 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MGC:28201 IMAGE:3989515"
/tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV."
/clone_lib="MCI_CCAP_Lu29"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product="2010107G23Rik protein"
/protein id="AAH24943.1"
/db_xref="GI:193542B9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGLLLVGLVYLVSHLSQR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="LocusID:69894"
/translation="MVRILANGEIVQDDDPRVRTTTQHRSSSSQQGFFNRGHGAPPGG
pgpRQQAGARLGAAQSPFSDLNRQLVNNGFPQWHLGNHVVEPVTSILLLFLLMMLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="2010107G23Rik"
/db_xref="LocusID:69894"
/db_xref="MGI:1917144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="CZECH II"
/db_xref="taxon:10090"
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NES NUZNY, D. Marie. Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Ballen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Balair, J., Blankenburg, S., Buth, P., Barnetad, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Barnetad, M., Benahmed, F., Cardenas, V., Carter, K., Cavacos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Chacko, J., Chavez, D., Derland, C., Dederich, D., Derland, C., Cockell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Chacko, J., Chavez, D., Derland, C., Dederich, D., Derland, C., Dederich, D., Derland, C., Derson, S., Dermo, C., Ding, Y., Dinh, H., Divya, K., Davyla, K., Bagn, A., Balls, T., Fan, G., Pernandez, S., Finley, M., Flagg, M., Fortes, I., Poster, M., Foster, P., Fernandez, S., Finley, M., Flagg, M., Fortes, I., Foster, M., Guevaza, M., Genrea, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Genrea, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Genrear, M., Guevaza, M.
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Rattus norvegicus (Norway rat)
Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC116233.7 GI:23101097
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On Sep 18, 2002 this sequence version replaced gi:21738715.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence ontigs will be indicated in the feature table.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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10939
273286
273386
274619
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Center clone name: CH220-95117
Center clone name: CH220-95117
Center clone name: CH220-95117
Center clone name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 234606 bases at least Q30
Consensus quality: 237265 bases at least Q30
Consensus quality: 238934 bases at least Q20
Estimated insert size: 264374; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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9666. .10838
/note="wgs_end_extension
clone_end:Sp6"
                                                                                /note="wgs_end_extension
clone_end:Sp6"
                                                                                                                                                                                        /clone="CH230-95L17"
                                                                                                                                                                                                                      /mol_type="genomic DNA
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                               organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                      10838: contig of 10838 bp in length
10938: gap of unknown length
279285: contig of 262347 bp in length
279385: gap of unknown length
274618: contig of 1233 bp in length
274718: gap of unknown length
274718: gap of unknown length
275924: contig of 1206 bp in length
                                                                                                                                                                                                                                                       _type="genomic DNA"
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                                                                                              GTCCGTTGGTTCCCGAGATACTTTTAGGTGGTATGGGGCCTGCATTAAGTGGCACAAAAT 781
                              CAGAGCAAGAAAGCGATGCCCTTCCCAATTCTCTCA
                                                                TCCCATGTTTTTCTGGAATGTTTTTAGGGGACATAGGGTCTCCATTACAAAGCAC-AAGC 227351
                                                                                                                                C----CGCTGCAGGAGGCAGAGGGACTCTCTGGGCCAGCATTGCTGAAAAAAATAG-AG
                                                                                                                                                              ĠĠĠAGCTŤĠĠĠŦĠŤĠĊ---TCĀĠĠŤĀŤĠĀŤĠGACĠŦĠAĠACĊĠŦĠĀĠŦĠŦAĠATĊŤŤĊĊĊ 227463
                                                                                                                                                                                                                                  GGGGATCTGGTGCTTGAAGGTATGATCAGAGAGGGGACCACAGGTGTGTTTTCCC
                                                                                                                                                                                                                                                                  GAGGCAGGCAGTGTTCAGTAGGATCGACTGGG-CTTCGAATGAGATCACGCACAGGGGGA
                                                                                                                                                                                                                                                                                                                                    CTTGTGGGTCTGGTGTGTGTCTCACCTGAGCCAGCGGTGACCTCCAGGGCCTCAT
                                                                                                                                                                                                                                                                                                                                                          CTGGTTGGCCTTGTCTACCTGGTGTCCCCACCTGAGTCAGCGGTGACCTCTGAGGGCTGAT
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\GAGTAAGAAAGGCTTAGTATGTTGTATTCTCCCA
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RESULT 15 AC111675/c

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                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                             Muzny, U. Marle, M. Medrocks, S. Main, A. Maguland, V., Allen, C., Allen, C., Allen, H., Alabrocks, S., Amin, A., Anguland, D., Anyalebechi, V., Aoyagi, A., Ayodej, M., Baca, E., Baden, H., Anyalebechi, V., Aoyagi, A., Ayodej, M., Baca, E., Baden, H., Balawin, D., Bandaranaike, D., Barber, M., Barnstead, M., Beahmed, F., Balawin, D., Bandaranaike, D., Barber, M., Barnstead, M., Beahmed, F., Balawin, D., Barder, M., Barnstead, M., Beahmed, F., Balawin, D., Barder, M., Balawin, M., B
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                  Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 240657)
Rat Genome Sequencing Consortium.
Direct Submission
                                                                                                                                                                      Worley, K.C.
Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unordered pieces.
AC111675
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*NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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236912
238256
238356
239506
239606
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/note="clone_boundary
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/db_xref="Laxon:10116"
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236911: gap of unknown length
238255: contig of 1344 bp in length
238355: gap of unknown length
239505: contig of 1150 bp in length
239605: gap of unknown length
239605: gap of unknown length
240657: contig of 1052 bp in length.
                                                           sequence:BH363875"
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of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:24818892.
The sequence in this sequence version replaced gi:24818892.
The sequence in this assembly is a combination of EAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature

Center project name: GMVI
Center clone name: CH230-48G14
Center clone name: CH230-48G14
Center clone name: CH230-48G14
Center clone name: CH230-48G14
Center clone name: Atlas 3.0;
Assembly program: Atlas 3.0;
Consensus quality: 228178 bases at least Q40
Consensus quality: 231963 bases at least Q30
Consensus quality: 231193 bases at least Q20
Consensus quality: 231139 bases at least Q20
Estimated insert size: 237555; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

B &	P 62	D 89	B 8	90 VQ	Å &	B 8	B 8	B 8	B 8	B 8	B 8	Query M Best Lo Matches
781 TCAGAGCAAGAAGCGATGCCCTTCCCAATTCTCTCA 817	721 GGTCCGTTGGTTCCCGAGATACTTTTAGGTGGTATGGGGCCTGCATTAAGTGGCACAAAA 780	661 CCTTTGTGTTAAGCGTGAGGCAGAGGGAGACGTTAGTCCAAGCATTTCCAAAGTGTGGGTG 720	601 AGGGATCTGGTGGTGCCTTGAAGGTATGATCAGAGAGGGGACCACAGGTGTGTGT	541 TAGGGGTGGGTTTGAGAGGGACTTGCTGGGGCCTTGGTGAGAGCAGGCATATTTGG 600	481 CCTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTGACCTCTGAGGGCTGA 540	421 GCCGGTGACCTCCATCCTGCTCCTCCTCCTGCTCATGATGCTTGGTGTTCGTGGCCTCCT 480	361 CAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGA 420 	301 CCCCGGCAGCAGGCAGGTGCCAGGCTGGGTGCTGCTCAGTCCCCCTTCAATGACCT 360	242 AGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCCCCCAGGGGGGTCCT-GG 300	182 GGGGAAATCGTGCAGGACGACCCCCGAGTGAGGACCACTACCCAGCCACCAAGAGGT 241	123 CTGGTGCAGCCCATCAGGGACCCACAGCGCCT-GGGAGGATGGTGCGGATCTTGGCCAAT 181	Query Match 24.7%; Score 294; DB 2; Length 240657; Best Local Similarity 71.6%; Pred. No. 4.4e-62; Matches 499; Conservative 0; Mismatches 181; Indels 17; Gaps 8;

Search completed: August 22, 2004, 02:37:28 Job time : 4696 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2004, 16:20:58 ; Search time 514 Seconds (without alignments) 9851.852 Million cell updates/sec

Title: Perfect score: US-10-001-885-31 1192

Sequence: aaaccgcctggagccgccgg.....gaagaggacacacggaaccc 1192

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters:

6747726

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries Maximum Match 100%

Database N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
9: geneseqn2003cs:*
10: geneseqn2003cs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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668	2269 577 355	461 986 420	365 612	1165 550 587 643	1192 1108 11049 1049 1049	Length
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ABS67265 ABT04062	ABT07649 ABX92021 ABX92192	AAS64819 ABT07559 ABT07560 ABT13409 ABT07648	ABX92251 ABX92250	AAS64820 AAF82505 AAS64821 ABN87819 ARY74673	ABN87820 ABL90057 AAV59458 ABS73545 ACD8268 ABZ11212	ð
5 Breast 2 Human	9 Human 1 Lung s 2 Human	AA864819 UNA ENCOG Abt07559 Human bre Abt07560 Human bre Abt13409 Breast sp Abt07648 Human bre	000	Aas64820 DNA encod Aaf82505 Human bre Aas64821 DNA encod Abn87819 Human ova Abr87817 Human cDN	20000000	Description

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4.8	4 .8	4.8	4.9	5.0	5.0	5.0	5.1	5.1	5.1	5.2	5 . 2	5. 2	5.3	υ. Έ	5.3	5. 3	σ. ω	5.4	5.4	5. 4	5. 5	
665	2910	1495	510	816	464	1623	1545	800	422	601	879	716	652	1206	657	626	536	666	1400	766	737	
7	σ	7	σ	σ	ψ	σ	σ	7	4.	Q	7	σ	σ	σ	7	σ	σ	σ	თ	თ	7	
ABX92249	ABN87829	ABX92216	ABN87806	ABS67268	ABV03810	AAD39107	ABX91992	ABX92232	AAL15924	ABV83649	ABT13356	ABT04069	ABS67291	ABT07562	ABX92246	ABN87873	ABT07561	ABN87812	ABT07680	ABT07679	ABT13319	
Abx92249 Human ova	Abn87829 Human ova	Abx92216 Human ova	Abn87806 Human ova	Abs67268 Breast sp	Abv03810 Human pro	Aad39107 Human lun	Abx91992 Lung spec	Abx92232 Human ova	Aal15924 Human bre	Abv83649 Human bre	Abt13356 Breast sp	Abt04069 Human ova	Abs67291 Breast sp	Abt07562 Human bre	Abx92246 Human ova	Abn87873 Human ova	Abt07561 Human bre	Abn87812 Human ova	Abt07680 Human bre	Abt07679 Human bre	Breast	

ALIGNMENTS

RESULT 1 ABN87820

ABN87820 standard; cDNA; 1192 腹

ABN87820;

12-AUG-2002

(first entry)

Human ovary specific nucleic acid SEQ ID NO:31.

Human; ovary specific nucleic acid; OSNA; ovary specific protein; OSP; ovary specific gene; OSG; ovarian cancer; immune response; metastasis; chromosome 10; gene; ss.

Homo sapiens.

WO200240535-A2

23-MAY-2002.

20-NOV-2001; 2001WO-US045011.

20-NOV-2000; 2000US-0252061P. 27-NOV-2000; 2000US-0253257P.

(DIAD-) DIADEXUS INC.

Salceda S, Macina RA, Recipon H, Cafferkey R, Sun Y, Liu

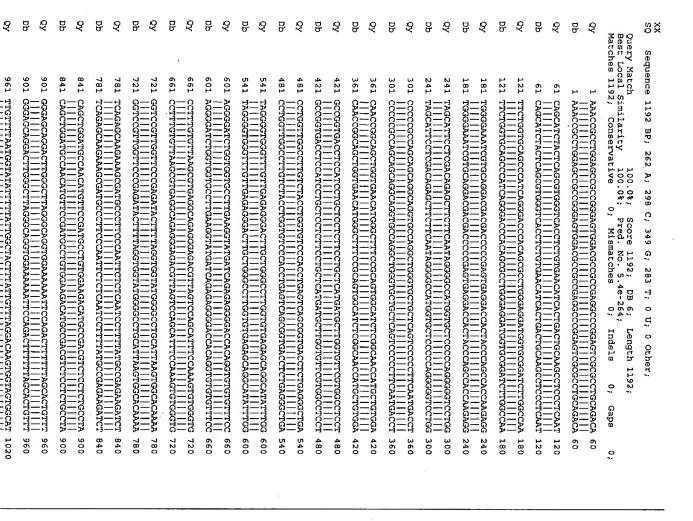
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WPI; 2002-471617/50.

New ovary specific genes and proteins, useful as a vaccine for treating patients with ovarian cancer, or for diagnosing and monitoring the presence and metastases of ovarian cancer in a patient.

Claim 1; Page 173-174; 260pp; English.

ABN87790 to ABN87882 represent human ovary specific nucleic acid (OSNA) sequences, and ABB79297 to ABB79370 represent ovary specific protein (OSP) sequences from the present invention. OSNA and OSP sequences have cytostatic activity, and can be used in vaccine production and gene therapy. An antibody that specifically binds to an OSP can be used for treating a patient with ovarian cancer, particularly for inducing an immune response against the ovarian cancer cell expressing the OSNA or OSP. The OSNAs and OSPs can also be used for diagnosing and monitoring the presence and metastases of ovarian cancer in a patient



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1141
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                                                                    CGCCCCAATTCCCCCCAAATTTTTGACAAAATGAAGAGGACACACGGAACCC
        CGCCCAATTCCCCCCAAATTTTTGACAAAATGAAGAGACACACGGAAACCC
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 1192
               1192
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ABL90057 standard; cDNA; 1108

24-MAY-2002 (first entry) polynucleotide SEQ ID NO 619

Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder neurological disease; infection; human; secreted protein; gene; ss. disorder;

Homo sapiens.

WO200190304-A2

18-MAY-2001; 2001WO-US016450

19-MAY-2000; 2000US-0205515P

(HUMA-) HUMAN GENOME

Birse CE, Rosen CA;

WPI; 2002-122018/16.

Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders.

Claim 4; SEQ ID NO 619; 2081pp + Sequence Listing; English

The invention relates to novel genes (ABL89449-ABL90853) and proteins CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic CC ansemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing (e), (e) neurological diseases such as myocardial ischaemias; (d) wound healing (f), (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) CC infectious. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly cfrom WIPO at ftp.wipo.int/pub/published_pct_sequences

중 음 성 뫄 8 δ 8 5 ద 8 밁 Ś 8 8 밁 맒 문 8 В 5 片 8 뭐 S Query Match
Best Local Similarity
Matches 1059; Conserv Sequence 1108 315 915 841 855 781 735 661 675 601 615 541 555 481 495 421 435 361 375 301 241 181 195 121 961 975 106 795 721 61 75 15 CATGTTCCGATGCCTGTGGAAGACATGCCGACGTCTCCTCTGCCTAGGGAGCAGGACTTG TTGAGAGGGACTTGCTGGGCCTTGGTGTGAGAGCAGCATATTTGGAGGGGATCTGGTGG recreate transfer of the second secon TGAACATGGGCTTTCCGCAGTGGCATCTYGGCAACCATGCTGTGGAGCCGGTGACCTCCA TGAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGAGCCGGTGACCTCCA AGGCAGGTGCCAGGCTGGGTGCTCAGTCCCCCTTCAATGACCTCAACCGGCAGCTGG AGGAYGACGACCCCGAGTGAGGACCACTACCCAGCCACCAAGAGGTAGCATTCCTCGAC AGGACGACGACCCCCGAGTGAGGACCACTACCCAGCCACCAAGAGGTAGCATTCCTCGAC ATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAATGGGGAAATCGTGC ATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAATGGGGAAATCGTGC CGCCGGGAGTGGACGCCGCCGAGGCCCGGAGTCGCGCCTGCAGACACACAGCATCTACTCAG GGCTTAGGGCAGGTGGAAAAAATTCCAGACTTTTTTAGCACTGTTTTTTGTTTTAATGGTA CGAGATACTTTTAGGTGGTATGGGGCCTGCATTAAGTGGCACAAAATCAGAGCAAGAAAG TTGAGAGGGA TCTACCTGGTGTCCCACCTGAGTCAGCGGTGACCTCTGAGGGCTGATAGGGGTTGGGTTTG TCCTGCTCCTCCTGCTCATGATGCTTGGTGTTCGTGGCCTCCTGGTTGGCCTTG CGATGCCCTT CGAGATACTTTTAGGTGGTATGGGGCCCTGCATTAAGTGGCACAAAATCAGAGCAAGAAAG GGCTTAGGGCAGGTGGAAAAATTCCAGACTTTTTTAGCACTGTTTTTGTTTTAATGGTA CGATGCC 89.0%; ilarity 99.6%; Conservative B₽; 234 A; ctrectes certes de la company 274 C; 4; Score 1061.4; Pred. No. 5.5e 4; Mismatches 324 <u>،</u> 271 4; DB 6; .5e-234; les 0; ij. 0 U; 6; Indels Length 1108; 5 Other; 0; Gaps 1034 900 600 540 480 420 180 194 134 60 960 974 840 854 660 674 614 554 494 434 360 374 300 314 240 254 914 780 794 720 0

> 음 성 1021 1035

AAV59558 standard; DNA; 1049 ₽**P**

AAV59558;

06-JAN-1999 (first entry)

secreted protein gene 48 clone HFCAI74.

RESULT 3
AAV552
ID AAV55
XX AAV5
XX AAV5
XX AAV5
XX AAV5
XX AAV5
XX AAV5
XX Huma
XX Home
XX O6-1
PF C7-1
PR C7-1-1
PR Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obseity, osteoclast; thymus; osteoprosis; arthritts; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens.

W09839448-A2

06-MAR-1998; 98WO-US004493

97US-0038621P

07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 11-APR-1997 23-MAY-1997 07-MAR-1997; 07-MAR-1997; 07-MAR-1997; 07-MAR-1997 97US-0040336P 97US-0040334P 97US-0040333P 97US-0040163P 3-0040161P. 3-0040162P.

97US-0040626P 97US-0043311P 97US-0043313P 97US-0043313P 97US-0043568P 97US-0043568P 97US-0043576P 97US-0043578P 97US-004367P 97US-004367P 97US-004367P 97US-004367P 97US-004367P 97US-004367P 97US-004750P 97US-004750P 97US-004750P 97US-004758P 97US-004758P

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Ruben SM, Rosen CA
Bednarik DP, Endre
Ferrie AM, Duan R,
Moore PA, Shi Y,
                                                                                                                                                                  23-MAY 1997
22-AUG-1997
 New isolated human genes and the secreted polypeptide(s) they encode
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P, Endress
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                                                                   CA, Fischer CL, Soppet DR, Carter KC;
dress GA, Yu G, Ni J, Feng P, Young PE,
R, Hu J, Florence KA, Olsen HS, Ebner!
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Best Local Similarity 99.3%;
Matches 1027; Conservative
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TTTCCAAAGTGTGGGTGGGTCCGTTGGTTCCCGAGATACTTTTAGGTGGTATGGGGCCTG
                                         ACCTCTGAGGGCTGATAGGGGTGGGTTTGTTGAGAGGGACTTGCTGGGCCTTGGTGTGAG
                                                                                                                                                                                                         TGTTCGTGGCCTCCTCGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTG
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RESULT 4
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07-MAR-1997,
07-MAR-1997,
11-APR-1997,
11-APR-1997, Human; ss; gene; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn; nervous system disorders; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive; preservative; nutritional. ABS73545 08-SEP-1998; 16-JUL-2002 US6420526-B1 Human 15-JAN-2003 ABS73545; 1004 sapiens 944 841 884 781 824 CDNA 721 764 GACGTCTCCTCTGCCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGA standard; AAAAAAAAAAAA 1077 CTTTTTTAGCACTGTTTTTGTTTTAATGGTATATTTTTATTGGCTACTTTATTGTTTAGG TTATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGTCC CATTAAGTGGCACAAAATCAGAGCAAGAAAAGCGATGCCCTTCCCCAATTCTCTCAATCCTT AAAAAAAAAAAAA 1034 CTTTTTAGCACTGTTTTGTTTTAATGGTATATTTTATTGGCTACTTTATTGTTTAGG CATTAAGTGGCACAAAATCAGAGCAAGAAAGCGATGCCCTTCCCAATTCTCTCAATCCTT #1 for (first 98US-00149476 novel secreted S-0030621P S-0040162P S-0040163P O0401334P S-0040334P S-0040334P S-00403312P S-0043312P S-0043312P S-0043313P S-0043313P S-0043314P S-0043314P S-0043314P S-0043314P S-0043314P S-0043314P S-0043314P S-0043568P S-004568P S-004568 cDNA; entry) 1049 ВP protein gene 48. 1063 1003 900 960 943 840 883 823 780 11-APR-1997
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23-MAY-1997
23-MAY 9703-0047492P 9703-0047501P 9703-0047501P 9703-0047501P 9703-0047582P 9703-0047582P 9703-0047583P 9703-0047583P 9703-0047583P 9703-0047589P 9703-0047593P 9703-0047593P 9703-0047593P 9703-0047593P 9703-0047593P 9703-0047593P 9703-0047593P 9703-0047593P 9703-004751P 9703-0047613P 970

97US-0043671P. 97US-0043672P. 97US-0043674P.

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The invention relates to an isolated protein that is one of 186 human CC secreted proteins, given in the specification. The protein is used in a condition in e.g. in the specification. The protein is used in a condition in e.g. humans, mice, rabbite, goats, horses, cate, dogs, chickens or sheeps. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, composed or treated include aniogenesis, nervous system disorders e.g. Alzheimer's disease, can also perfections caused by bacteria, viruses and fungi and coular disorders e.g. cerebral ischaemia, components, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used to aid wound confidency to maintain organs before transplantation, for supporting cell conformaty tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used to aid wound confidency to primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used to aid wound confidency to the primary tissue, to repenerate tissues and in chemotaxis. The components. The present sequence represents a condition a gene encoding one of the novel human secreted proteins of the invention. Note: other manual confidency and confidency and
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22-AUG-1997;
05-SEP-1997;
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05-SEP-1997;
12-SEP-1997;
02-OCT-1997;
06-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC; Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Gerrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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ACD82688 standard; CDNA; 1049

(first entry)

cDNA sequence #48 containing coding region of a human secreted protein.

Human; secreted protein; hyperproliferative disorder; leukaemia; breast cancer; wound; reproductive disorder; blood-related disorder; haemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplassia; wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis; graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma; viral infection; bacterial infection; fungal infection; Allory; sepsis; renal disorder; kidney failure; cardiovascular disorder; cytostatic; angina pectoris; cerebral ischaemia; congenital heart defect;

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-00476 -00476 -00476 -00476 -00476 -00476 -00476 -00476 -00488	97US-0043671P 97US-0043671P 97US-0043674P 97US-0047500P 97US-0047500P 97US-0047503P 97US-0047503P 97US-0047583P 97US-0047583P 97US-0047586P 97US-0047586P 97US-0047589P 97US-0047590P 97US-0047590P 97US-0047594P 97US-0047594P 97US-0047595P 97US-0047595P 97US-0047595P 97US-0047595P		iisorder; neurological disorder; Alzheimer's disease; lisease; inflammation; Crohn's disease; vulnerary; sive; antibacterial; haemostatic; thrombolytic;; reuroprotective; thyromimetic; antiallergic;; virucide; fungicide; anti-HTV; nephrotropic; antianginal; tive; cardiant; nootropic; antiparkinsonian; cory; gene; ss. Al.

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16-JUL-1997
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16-JUL-1997
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22-AUG-1997
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GREENE J M.
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FINTENCE K A.
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Soppet
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    Carter
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    Bednarik DP;
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The present invention relates to the isolation of novel human secreted proteins and the polynuclectide sequences encoding them. The invention CC producing human secreted proteins are useful for producing human secreted proteins. The polypeptide and polynuclectide sequences for the secreted proteins are useful for preventing, treating, CC ameliorating or diagnosing medical conditions such as hyperproliferative cdisorders (e.g. leukaemia or breast cancers) wounds, reproductive cc disorders, blood-related disorders (e.g. haemophilia or cthymic hypoplasia), immunodeficiencies (e.g. wiskott-Aldrich syndrome or cthymic hypoplasia) autoimmune disorders (e.g. wiskott-Aldrich syndrome or contitue sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma), contitue sclerosis, cerebral ischaemia or congenital heart defects), renal consorders (e.g. kidney failure), cardiovascultar disorders (e.g. anglina pectoris, neurological disorders (e.g. Alzheimer's disease or conformations), and inflammations (e.g. Crohn's disease). The colymerce data for this patent did not form part of the printed conformation, but was obtained in electronic format directly from the USPTO web site at segdata.uspto.gov/psipsDIDEntry.html
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Best Local Similarity
Matches 1027; Conserv
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J, Florence KA, Olsen HS, Fischer CL, Ebner
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, F
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RESULT 6
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05-MAR-2001; 2001US-00799451

05-MAR-2002; 2002WO-US005095

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Tang Xue / Wehrman TY, TA T, Zhou P, (, Yang Y, Ma n T, Wang J, Ma Goodrich RW, Asundi V, Z) Ma Y, Yamazaki V, Chen R, , Wang D, Drmanac RT; Zhang J, R, Wang ; 'n Zhao QA, , Ghosh M; Ren

WPI; 2002-759812/82.

New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet coagulation disorders.

Claim 1; SEQ ID NO 94; 1012pp + Sequence Listing; English

nucleotide sequence selected from any of 948 sequences (ABZ1119-CABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69894) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cellimaging, screening and for treating cellimaging, screening and for treating cellimaging, screening and for treating cellimaging and The invention relates to an isolated polynucleotide (I) comprising mucleotide sequences (ABZ11119ø

Sequence 562 BP; 95 A; 176 C; 174 G; 117 T; 0 U; 0 Other;

Similarity

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Length 562;

S 밁 당 Ś 밁 밁 밁 S Ś Ś 밁 δ 뮍 Š 밁 Ś Query Match
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Matches 562; 421 436 361 301 316 241 256 181 196 121 136 13 76 16 μ CCTGCTCCTCCTCCTCATGATGCTTGGTGTTCGTGGCCTCCTCCTGGTTGGCCTTGT GAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGAGCCGGTGACCTCCAT GAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGAGCCGGTGACCTCCAT GGCAGGTGCCAGGCTGGGTGCTCAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGT GGCAGGTGCCAGGCTGGGTGCTCAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGT GAGCTTCTTCAATAGGGGCCATGGTGCTCCCCCCAGGGGGTCCTGGCCCCCGCCAGCAGCA GGACGACGACCCCGAGTGAGGACCACTACCCAGCCACCAAGAGGTAGCATTCCTCGACA GGACGACGACCCCGAGTGAGGACCACTACCCAGCCAAGAGAGGTAGCATTCCTCGACA TCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAATGGGGAAATCGTGCA TCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAATGGGGAAATCGTGCA GCCGGGAGTGGACGCCGCGAGGCCCGGAGTCGCGCCTGCAGACACAGCATCTACTCAGC 47.1%; Scilarity 100.0%; F Score 562; DB; Pred. No. 2.800; Mismatches 0 Indels 0 Gaps 555 375 315 255 180 195 120 540 480 495 420 435 360 300 240 60

> ARSOLT 7
> AASSA AASSA
> XX HOME
> XX H 밁 S 30-MAR-2001; 2001WO-US008631. WO200175067-A2 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; DNA encoding 13-FEB-2002 AAS64820; AAS64820 standard; cDNA; 1165 11-OCT-2001 sapiens. 541 556 TGAGAGGGACTTGCTGGGCCTT 562 TGAGAGGGACTTGCTGGGCCTT novel human (first entry) diagnostic protein ВP 577

WPI; 2001-639362/73. 31-MAR-2000; 23-AUG-2000; (HYSE-) RT, HYSEQ INC ABG00633. 2000US-00540217. 2000US-00649167. Liu C, ĭ

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ID NO 624; 103pp; English

The invention relates to isolated polynucleotide (I) and polypeptide (II) csequences. (I) is useful as hybridisation probes, polymerase chain (C reaction (PCB) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polynucleotides are also used (in diagnostics as expressed sequence tags for identifying expressed (genes. (I) is useful in gene therapy techniques to restore normal (C useful for generating antibodies against it, detecting or quantitating a (II) is (II) and its binding partners are useful in medical imaging (C supplement. (II) and its binding partners are useful in medical imaging (II) (II) and its binding partners are useful for treating disorders (involving aberrant protein expression or biological activity. The (C diagnostics, forensics, gene mapping, identification of mutations (C diagnostics, forensics, gene mapping, identification of mutations (C amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic (C coding sequences of the invention. Note: The sequence data for this (C clectronic format directly from WIPO at the product of the involvence.) ftp.wipo.int/pub/published _pct_sequences

Sequence 1165 B₽; 247 A; 279 Ç 342 G; 297 H 0 U; 0 Other;

S Matches Query Match Best Local Similarity ATTTCTGGTGCAGCCCATCAGGGACCCACAGCGCC--TGGGAGGATGGTGCGGATCTTGG Conservative 38.2%; 0 Score 455.4; DB 5; Pred. No. 1.2e-94; 0; Mismatches 51; Indels 145; Length 1165; Gaps 176

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                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a breast tumour-associated protein. It was shown to have at least two-fold overexpression in breast tumour tissue. The invention relates to an isolated polypeptide comprising at least an immunogenic portion of a breast tumor-specific protein, or its variant that retains the ability to react with antigen-specific antisera. The breast tumour polymuncleotides, polypeptides and antibodies are useful for inhibiting development of breast cancer. The polymucleotides may be used to design primers and probes for detecting and monitoring breast cancer
                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                  AACCATGC-TGTGGAGCCGGTGACCTCCATCCTGCTCCTCCTTCCTGCTCATGATGCTTGG
                                                                                                                          CCAGGGGGTCCTGGCCCCGCCAGCAGCAGCAGGTGCCAGGCTGGTGCTGCTCAGTCC
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AAF82505 standard;

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466 361

TGTTCGTGGCCTCCTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTC-AGCGGT

524 419

ACCATGCTTGTGGAGCCGGTGACCTCCATCCTGCT-CTCTTCCTGCTCATGATGCTTGG

RESULT 9
AAS64821
ID AAS64821
ID AAS64821
AC AAS6
XX AAS6
XX AAS6
XX AAS6
XX DNA
XX Huma
XX Homo
XX Ho S В δ 뮍 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. Claim 1; SEQ ID NO 625; 103pp; English 30-MAR-2001; 2001WO-US008631. Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; AAS64821 standard; WO200175067-A2 DNA encoding 13-FEB-2002 (HYSE-) HYSEQ INC. 2001-639362/73. 540 580 480 525 420 TGGTCGTGGCCTNCTTCTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAATCAAGCGGT TGGG 543 TGTG 583 GACCTTTTGAAGGGCTGATANGGGGTGGGGTTTGTTGAAAAGGAACTTGCTGGGCCNTGG GACCTCT--GAGGGCTGATAGGG---GTGGGTTTGTTGAGAGGGGACTTGCTGGGCCTTGG Liu C, novel human diagnostic protein #625 (first entry) CDNA; Tang 587 579 539 479

The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the content of the inventory of the product of the inventory of the product of the inventory of the product of the product of the sequences of the inventory of the product of t ftp.wipo.int/pub/published_pct_

BP; 147 A;

106 C;

166 G; 168

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RESULT 10
ABN87819
ID ABN87819
XX ABN877
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XX ID-AU
XX Humar
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XX Humar
XX Ovary
KW Gene;
XX Homo
XX Ho 밁 S Ś S 당 밁 8 밁 Ś 맑 ঠ 밁 Ś 밁 ঠ 밁 8 밁 Matches 551; Query Match Human; ovary specific nucleic acid; OSNA; ovary specific protein; OSP; ovary specific gene; OSG; ovarian cancer; immune response; metastasis; gene; ss. 20-NOV-2000; 27-NOV-2000; Human ovary specific nucleic acid SEQ ID NO:30. Salceda 20-NOV-2001; 2001WO-US045011 23-MAY-2002. WO200240535-A2 Homo sapiens. 12-AUG-2002 ABN87819 standard; cDNA; 643 Local 1034 914 361 855 301 241 481 974 421 797 738 181 681 121 626 566 13 ß DIADEXUS INC Similarity Transarcasasasses coccacas sure reference control of transacci ranges 180 GGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTTTTTAGCACTGTTTTTTGTTTTAATGGT ATATTITTATIGGCTACTITATIGITITAGGACAAGIGGGTAGIGGCATICTATITATIGIG 1033 GGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTTTTTAGCACTGTTTTTGTTTTAATGGT CAGGTTCCGATGCCTGTGGAAGACATGCCGACGTCTCCTCTGCCTAGGGAGCAAGGACTT CATGTTCCGATGCCTGTGGAAGACATGCCGACGTCTCCTCTGCCTAGGGAGC-AGGACTT ATGCCCTTCCCAATTCTCTCAAATCCTTTTATGCCGAGAAGATTTCAAGTGGAAGCCCAA GATACTTTTAGGTGGTAATGGGGCCTGCATTAAGTGGCACAAAATCAGAGCAAGAAAGCG GATACTTTTAGGTGGT-ATGGGGGCCTGCATTAAGTGGCACAAAATCAGAGCAAGAAAGCG 796 CAGAGGGAGACGTTAGTCC--AGCATTTCCAAAGTGTGGGTGGGTCCGTTGGTT-CCCGA -TATGATCAGAGAGGGG-ACCACAGGTGTGTGTTTCCCCCTTTGTGTTAAGCGTG---AGG TTGCTGGGCCTTGGTGTGAGAGCAGGCATATTTGGAGGGGATCTGGTGGTGCCTTGAAGG TTGCTGGGCCTTGGTGTGAGAGCAGGCATATTTGGAGGGGATCTGGTGGTGCCTTGAAGG 625 ATGCCCTTCCCAATTCTCTC-AATCCTTTTATGCCGAGAAGATCTCAGCTGGATG-CCAA Macina RA, Conservative 2000US-0252061P. 2000US-0253257P. (first entry) 36.5%; Recipon H, Score 434.6; DB 5; Pred. No. 5.5e-90; Nd ematches 24; ₿₽. Cafferkey æ Indels Sun Length Ķ Liu. 12; ü 120 854 240 913 360 737 680 480 973 420 60 9

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Best Local Similarity 96.1%;
Matches 519; Conservative
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                                                                                                                       ATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACGTCTCCTCTG
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                GGTTCTCCCGGCCCAATTCCCCCCAAATTTTTGACAAAATGAAGAGGGACACACGGAACCC 1192
                                                                            AAAAAAAAAAAAAACCTGTGGGGGGTTACCCCGGGGCCAAAGGGGGGCCCCCGGGGGGAATGT 1132
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GGTTCTCCCGCCCAATTCCCCCCAAATTTTTGACAAAATGAAGAGACACACGGAACCC
                                                           AAAAAAAAAAAAGCTGTGGGGGTTACCCGGGGCCAAAGGGGGGCCCCGGGGGGAATGT
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Pred. No. 1.5e-89;
0; Mismatches 12;
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differential expression profile; aggressive CC-RCC tumour type, non-aggressive CC-RCC tumour type; clear cell renal carcinoma; gene expression profiling; tumour tissue; gene; ss. Homo sapiens.

WO200279411-A2

10-OCT-2002

29-MAR-2002; 2002WO-US009576

29-MAR-2001; 2001US-0279411P

(VAND-) VAN ANDEL INST

Rhodes D, BT, 3

New microarray, comprising a matrix of cDNA probe from a set of probes immobilized to a solid surface in predetermined order, useful in the prognosis of patients with clear cell renal carcinoma.

Claim 1; SEQ ID NO 459; 179pp; English.

The present invention relates to a microarray comprising a matrix of at CC least one cDNA probe from a set of probes immobilised to a solid surface CC in a predetermined order, where a row of pixels corresponds to replicates CC of one distinct probe from the set. The probes are complementary to CC compared to non-aggressive types of clear cell renal carcinoma (CC-RCC) CC and that hybridise to the probes under high stringency conditions. The microarray is useful for the prognosis of patients with CC-RCC, wherein CC aggressive and non-aggressive CC-RCC tumour types are characterised by CC differential expression profiles of genes that hybridise with one or more CC probes immobilised on the microarray. The arrays are useful for gene CC expression profiling of tumour and normal tissues. The presents equence CC expressents a human cDNA sequence differentially expressed in aggressive cy.

Sequence 517 BP; 166 A; 154 C; 90 G; 107 T; 0 U; 0 Other;

Conservative

31.2%;

Length 517; Indels 120;

Gaps

8 당 Ś B Š 뮍 Ş 밁 δ 밁 밁 8 Query Match
Best Local Similarity
Matches 514; Conserv 278 672 338 612 398 552 457 492 517 432 218 732 TTGTTGAGAGGGACTTGCTGGGCCTTGGTGTGAGAGCAGGCATATTTGGAGGGGATCTGG TTGTTGAGAGGGACTTGCTGGGCCTTGGTGIGAGAGCAGGCATATTTGGAGGGGATCTGG TCCCGAGATACTTTTAGGTGGTATGGGGGCCTGCATTAAGTGGCACAAAATCAGAGCAAGA TGGTGCCTTGAAGGTATĠATCAGAGAGGGGACCACAGGTGTGTGTGTTTCCCCCTTTGTGTTA 671 TCCCAAGATACTTTTAGGTGGTATGGGGCCTGCATTAAGTGGCACAAAATCA------Score 372.2; DB 7; Pred. No. 1.2e-75; 0; Mismatches 3; 279. 791 219 339 611 399 551 458 491 167

RESULT 11
ABX74673/c
ID ABX74673 standard; cDNA; 5:
XX
AC ABX74673;
XX
DT 21-WAR-2003 (first entry)
XX
DT 21-WAR-2004 sequence #128 d.
XX

517

ВP

(first entry)

#128 differentially

expressed

ij

CC-RCC

S

792

AAGCGATGCCCTTCCCCAATTCTCTCAATCCTTTATGCCGAGAAGATCTCAGCTGGATGC

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RESULT 12
ARX92251
ID ARX92
XX ABX92
XX ABX92
XX Human
XX Human
XX Homo
XX Homo
XX Homo
XX 13-FE
XX 13
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The invention relates to a new isolated nucleic acid termed ovarian specific nucleic acid (OSNA) comprising: (a) a nucleic acid molecule that encodes any of 53 fully defined protein sequences appearing as ABU61018-ABU61070 (termed ovarian specific proteins, OSP); (b) any of 76 fully defined nucleotide sequences appearing as ABS92167-ABS92662; or (c) a sequence having at least 60% sequence identity to the nucleic acid molecule of (a) or (b). Also included are a method for determining the presence of an ovary specific nucleic acid (OSNA) in a sample, a vector comprising an OSNA, a host cell comprising the vector, an isolated OSP polypeptide, an anti-OSP antibody or fragment, a method for determining the presence of an ovary specific protein in a sample and a vaccine comprising an OSP or OSNA. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous disease in ovary tissue. The present sequence is an OSNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated OSNA nucleic acid and encoded polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous diseases in ovarian tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 185-186; 224pp; English.
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Sun Y, Liu C;
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15-FEB-2001; 2001US-0268834P.
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DB; ABU61063.
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ARESULT 13
ARE92250
ID ARE992250
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                      New isolated OSNA nucleic acid and encoded polypeptide, useful identifying, diagnosing, monitoring, staging, imaging and treat ovarian cancer and non-cancerous diseases in ovarian tissues.
                                                                                                                    P-PSDB;
                                                                                                                                                                                                             Salceda
                                                                                                                                                                                                                                                                                                      13-FEB-2001; 2001US-0268290P.
15-FEB-2001; 2001US-0268834P.
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                                                                                                                                                                                                                                                          (DIAD-) DIADEXUS INC.
                                                                                                                    2003-120677/11.
)B; ABU61062.
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C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ovarian specific nucleic acid; OSNA; ovarian cancer; arian disease; gene therapy; vaccine; cytostatic;
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treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a new isolated nucleic acid termed ovarian CC specific nucleic acid (OSNA) comprising: (a) a nucleic acid molecule that CC encodes any of 53 fully defined protein sequences appearing as ABUGIO18-CC ABUGIO70 (termed ovarian specific proteins, OSP); (b) any of 76 fully defined nucleotide sequences appearing as ABUGIO18-CC defined nucleotide sequences appearing as ABUGIO18-CC encled of (a) or (b). Also included are a method for determining the CC presence of an ovary specific nucleic acid (OSNA) in a sample, a vector CC comprising an OSNA, a host cell comprising the vector, an isolated OSP polypeptide, an anti-OSP antibody or fragment, a method for determining CC the presence of an ovary specific protein in a sample and a vaccine CC comprising an OSP or OSNA. The methods and compositions of the present cc comprising an OSP or OSNA. The methods and compositions, desping, cc imaging and treating ovarian cancer and non-cancerous disease in ovary tissue. The present sequence is an OSNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                               13-FEB-2002
                                                                                                                                  AAS64819
                                                                                                                                                                   AAS64819 standard; cDNA; 348 BP
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                                                                                                                                                                                                                                                                                                                                                                       AAAAAAAAAAAAAAGCTGTGGGGGTTACCCGGGGCCAAAGGGGGGGCCCCGGGGGGGAAT 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTTTTGTTTTAATGGTATATTTTATTGGCTACTTTATTGTTTAGGACAAGTGGTAGTG 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTTCCAGACTTTTTTAGCACT
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                                                                                                                                                                                                                                                                                             GTGGTTCTCCCGCCCAATTCCCCCCAAATTTTTGACAAA 1170
                                                                                                                                                                                                                                                                                                                                    ACAAAAAAAAAAAAAGGCGTGGGGGGAACCCCGGGGCCAAAGCCCTGTTCCCCGGGGTGACAT
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Pred. No. 1.5e-73;
0; Mismatches 53;
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

DNA encoding novel human diagnostic protein #623.

RESULT 15 ABT07559

ABT07559 standard; cDNA; 461

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BRARB

ABT07559;

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The invention relates to isolated polynuclectide (I) and polypeptide (II) creation (PCR) primers, oligomers, and for chromosome and gene mapping, cc and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed cc in diagnostics as expressed sequence tags for identifying expressed cc activity of (II) or to treat disease states involving (II). (II) is ceful for generating antibodies against it, detecting or quantitating a cc polypeptide in tissue, as molecular weight markers and as a food cc polypeptide in tissue, as molecular weight markers and as a food cc supplement (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders co involving aberrant protein expression or biological activity. The cc polypeptide and polymuclectide sequences have applications in cresponsible for genetic disorders or other traits to assess biodiversity cand to produce other types of data and products dependent on DNA and coding sequences of the invention. Note: The sequence data for this coding sequences of the invention. Note: The sequence data for this calcular did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at figure in the printed specification, but was obtained in celectronic int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                    Matches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 348 BP; 121 A; 94 C; 58 G; 75 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 623; 103pp; English.
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ATTTATTGTGACCTTTTCAATAAATAGATTTAAGTAAAA 1062
                                                                                                                                                                                                                               AGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTTTTTAGCACTGTTTTTG
                                                                                                                                                                                                                                                                          AGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTTTTTAGCACTGTTTTTG
                                                                                             TTTTAATGGTATATTTTATTGGCTACTTTATTGTTTAGGACAAGTGGTAGTGGCATTCT
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                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                13.3%; Score 159; DB 5; 1
100.0%; Pred. No. 1.1e-26;
rative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                            Query Match 6.3%; Score 75.6; DB 6; Length 461; Best Local Similarity 62.9%; Pred. No. 1.7e-07; Matches 117; Conservative 0; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides human breast specific coding sequences and proteins. These can be used in the diagnosis and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence is a coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New breast specific nucleic acids and proteins, useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissue, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                         Sequence 461 BP; 142 A; 84 C; 90 G; 145 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 179; 367pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salceda S, Macina RA,
Sun Y, Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; breast specific gene; breast specific protein; breast cancer; gene therapy; cytostatic; gene; ss.
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                                                                                       1166 ACAAAA 1171
                                                                                                                                                1106 CCAAAGGGGGGGCCCCGGGGGGAATGTGGTTCTCCCGCCCAATTCCCCCCAAATTTTTG 1165
                                                                                                                                                                                                451
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Sequence:
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Maximum Match 100%
Listing first 45 summaries
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11885.048 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Invitrogen. This sequence belongs to sequence cluster 5629.f For more information about this cluster, see http://www.genoscope.cns.fr/ http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSODP034CP12NP1&cluster=5629.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600	BP 191 9106 EWRY cedex - France BP 191 9106 EWRY cedex - France Bmail: segref@genoscope.cns.fr Bmail: segref@genoscope.cns.fr Tibrary was constructed by life Technologies a division of	Conserve Control National de Comiencade	Full-length cDNA libraries and normalization	1 (bases 1 to 1059)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoscomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	Homo sapiens (human)	EST.	BX420823.1 GI:30768055	BX420823	CSODF034YL23 3-PRIME, mRNA sequence.	BX420823 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone	BX420823 1059 bp mRNA linear EST 15-MAY-2003	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Torgan: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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/db xref="taxon:9606"
/db xref="taxon:9606"
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mol_type="mRNA"
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Matches 909
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                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMNILS4 row: i column: 19
High quality sequence start: 31
High quality sequence start: 31
High quality sequence stop: 841.
Location/Qualifiers
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3 ACCGCCTGGAGCCGCCGGAGTGGACGCCGCCGAGGCCCGGAGTCGCGCCTGCAGACACA
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1 (bases 1 to 1027)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                  Similarity
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                                                                                                               /clone lib="NIH MCC_120"
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/note="Torgan: pooled pancreas and spleen; Vector:
pcMv-SPORT5; Site 1: Not1; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5220570"
                                                                                                                                                                                                                                                                                          Lab
                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:15347012
                                                60.4%;
                                                                                                                                                                                                                                                                                       _host="DH10B"
                                o,
                                Score 719.6; DB 1
Pred. No. 3.6e-91;
0; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bp mRNA linear EST 29-AUG-2001 sapiens cDNA clone IMAGE:5220570 3',
                                                                DB 12;
                                  84;
                                  Indels
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                                  Gaps
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62

RESULT 3 BE904302 LOCUS DEFINITION		9						80		Ov 7	Db 3	9 9				Db 5	Qy 4	Db 6	8		Qy 3	B 4	•	ДУ 2		20/	Db 9	02/	Db .	Ą	ე ხ
BE904302 980 bp mRNA linear EST 20-OCT-2000 601494571F2 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896656 5', mRNA sequence.	66 CTTTTTAAGCACTGTGTTTGTTAATGGTATATTTTTTTTGGATACTTCAT 15	44 CTTTTTAGCACTGTTTTGTTTTAATGGTATATTTTTAT	26 GACGTCTCCTTGCCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAG	84 GACGTCTCCTCTGCCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAATTTCCAGA 9	.86 TATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTCCGAGGCCTGTGGAAGACATGCGC 12	25 TATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGC-C 8	246 TTANGTGGCACAAGAATCAGAAGCAAGAAAGCGATGCCCTTCCCAATTCTGTCAATCCTTA 187	stegcacaa-aatcagagcaagaaagcgatgcccttcccaatctctcaatc	.06 TCCAAAGTGTGGGTGGGTCGGTTGGTTCCCGAGATACTTTTAGGTGGTATGGGGCCTGCA 24	06 TCCAAAGTGTGGGTGGGTCCGTTGGTTCCCGAGATACTTTTAGGTGGTATGGGGCCTG	66 CAGGTGTGTTTTCCCCTTTGTGTTTAAGCGTGAGGCAGAGGGAGAGGCGTTAGTCCAGCATT 30	A COMPANDATA TOTAL TOTA	88 CAGCAIATITGAGGGAITCIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGG	86 TGAGGGCTGATAGGGGTGGGATTTGTTGAGAGGGACTTGCTGGGCCTTGGTAGTTGAGAG 42	31 TGAGGGCTGATAGGGGTGGG-TTTGTTGAGAGGGACTTGCTGGGCCTTGGTGTGAGAG 58	46 GTGGCCTCCTGGTTGGCCTTGTCTACCTGGTGTCCCACGTGAGTCAG	71 GTGGCCTCCTCGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGG	06 ARGCTGTGGAGCCGGTGACCTCCTCCTCCTCCTCCTCCTCATGATGCTTGGTGTT	creregaeccegreaccrecarccrecrecrecrecrearearecrreer		51 TCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTTCCGCAGTGGCATCTCGC	6 GGTCCTGGCCCCACGCCAGCAGCAGCAGGCAGGCAGGCTGGGTGCTGCCTCAGTCCCCCT 66	**************************************	236 AGARGET-AGCATICCTCGACARAGCTTC-TTCAATAGGGGCCAIGGTGCTCC-CCCAGGG 292 	46 CAATGGGGAAAATCGTGCCAGGATGGACGACCCCCGAGTGAGGACCACTACCCAGCCACCA 7	78 CAATGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACCACTACCCAGCCACC	06 CGGGCGCAGCCCCATGAGGGGACCCAACAGCGGCCTGCGAAGGATGGTCAGGATCTTGG	23 CTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATC		GOGTGGGTCACCTCTGTGAACATCACTGACTGCAAGCCTCCCTC	

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Best Local Similarity
Matches 796; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 980)

RS NHH-MGC http://mgc.nci.nih.gov/.

RS NHH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: ATCC
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLAM9689 row: n column: 17
    High quality sequence stop: 711.

ES
    Location/Qualifiers
    1 980
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CCTCTTCCTGCTCATGATGCTTGGTGTTCGTGGCCTCCTCGTGGCCTTGTCTACCT 501
                                                                                                                     GGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGAGCCGGTGACCTCCATCCTGCT
                                                                                                                                                                            TGCCAGGCTGGGTGCTCAGTCCCCCCTTCAATGACCTCAACCGGCAGCTGGTGAACAT 381
                                                                            GGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGGAGCCGGTGACCTCCATCCTGCT
                                                                                                                                                        TGCCAGGCTGGGTGCTCAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGTGAACAT
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/mol type="mRNA"
/mol type="mRNA"
/db xref="raxon.9606"
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/tissue_type="epithelioid carcinoma"
/lab_host="PH108 (phage-resistant)"
/clone_lib="NIH_MGC_70"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.1%; Score 716.2; DB 10; Length 99 94.6%; Pred. No. 1.1e-90; tive 0; Mismatches 38; Indels
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MEDLINE
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                                                                                                           Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-42, AT_rich#Low_complexity (matched compliment)
Seg primer: M13 Forward
POLYA=Yes.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene discovery
                                                                                                                                                                                                                                                                                                                                                              Genome Rés. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM675290 708 bp mRNA linear FUT-E-EJO-ahr-n-23-0-UI-S1 UI-E-EJO Homo sapiens cDNA UI-E-EJO-ahr-n-23-0-UI 3', mRNA sequence.

BM675290
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/organism="Homo sapiens"
/mol type="mark]
/mol type="mark]
/db xref="reaxon:9606"
/clone="UI-E-EJO-ahr-n-23-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
                                                                                               Location/Qualifiers
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                                                      GACTTGCTGGGCCTTGGTGTGAGAGCAGCATATTTGGAGGGGATCTGGTGCCTTGA 622
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                                                                                                                                                                               TTCCCAATTCTCAATCCTTTTATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTCC
                                                                                                                                                                                               TTCCCAATTCTCTCAATCCTTTTATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTCC
                                                                                                                                                                                                                                            TTTTAGGTGGTATGGGGCCTGCATTAAGTGGCACAAAATCAGAGCAAGAAAGCGATGCCC
                                                                                                                                                                                                                                                                TTTTAGGTGGTATGGGGCCTGCATTAAGTGGCACAAAATCAGAGCAAGAAAGCGATGCCC
                                                                                                                                                                                                                                                                                                         AGGTATGATCAGAGAGGGGACCACAGGTGTGTGTGTTTTCCCCTTTTGTGTTAAGCGTGAGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="fetal and adult"
//lab host="DH10B (Life Technologies) (T1 phage resistant)"
//clome_lib="U1-E-EJ0"
//clome_lib="U1-E-EJ0"
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EJ0 is a subtracted CDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonuclectide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGAATCAGAG; lens, CGATTAGCGA; eye anterior segment,
AAATGCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI).
TAG_ESEQ=GTCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.4%;
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	/ 22 AGTGGACGCCGGCCGGAGTCGCGGAGTCGCAGACACAGCATCTACTCAGCGTGGGT 81	Ş
	Query Match 57.4%; Score 684.8; DB 12; Length 688; Best Local Similarity 99.7%; Pred. No. 3.3e-86; Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
	ORIGIN Cracking code 025. Note: this is a NIH_MGC Library."	ဋ
	ncoky site is destroyed upon cloning). Average insert size is 1.5 kb, insert size range 1.2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics	
	source anonymous pool of spleen and pancreas from 28 your male. Library is oligo-dT primed and directionally cloned	
	/ CIOHE ILDE WIR POOLED FOR AND SPICEN; Vector: /note="Organ: Pooled FACT: Site 3: Fooby (Assertowed): DNA	
	/lab_host="NHTU MCC 120"	
	/db xref="taxxx: /clone="tMAGE:520570"	
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	Plate: LLAW11554 row: i column: 19 High quality sequence stop: 688.	
	LLNL at:	
	ne d	
	cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
	gapbs-r@mail.nih.gov rocurement: Life Technol	
	Contact	Ω Ω
	AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC)	
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	Motorous (Thomasters Constitutes Vietobusts)	Ģ
	EST.	2 25 1
	ACCESSION BI521387 VERSION BI521387:1 GI:15346179	≤≱
	DEFINITION 63361177F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5220570 5',	<u> </u>
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12220 row: i column: 16
High quality sequence stop: 585.
Location/Qualifiers
1. .937
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Homo sapiens
Elkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Elkaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 937)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
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/lab host="DH10B (phage-resistant)"
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/clone_lib="NIH_MGC_71"
/clone_lib="NIH_MGC_71"
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
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BX455674.1 GI:31022729
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 931)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-lenorh cDNA libraries and normalization
                                                                       Homo sapiens (human)
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5629.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAK043BH05NM1kcluster=5629.f. Contact
Feng Liang Email: fliang@nifetech.com URL:
http://fulllength.invitrogen.com/INVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0BAK043BH05NM1.
Location/Qualifiers
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          ATTAAGTGGCACAAAATCAGAGCAAGAAAGCGATGCCCTTCCCCAATTCTCTCAATCCTTT
                                                                                                    TTCCAAAGTGTGGGTGGGTCCGTTGGTTCCCCGAGATACTTTTAGGTGGTATGGGGCCTGC
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                                                                                                                                                                                                                                                                                                                                    GTGTTCGTGGCCTCCTCCTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/mb_xref="taxon:9606"
/clone="CSODF034YL23"
/tissue_type="FETAL BRAIN"
/tissue_type="FETAL BRAIN"
/clone_lib="nomo sapiens FETAL BRAIN"
/clone_lib="nomo sapiens FETAL BRAIN"
/clone_"Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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94.3%;
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Pred. No. 4.5e-86;
0; Mismatches 40
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7 TATUTCCCCCACGAMANATCTCCACCTCCATCCCATCCCACC 188 5 AGGTCTCCCTCCTACCTACGAGCACACCTTGCACTCCACCCCACC 944 7 AGGTCTCCCTCCTCCTACGAGCACACCTTGGGTCTTACGAGCAGAGTGGAAAAAATTCCACAC 128 7 TATTTTAGCACTGTTTTGTTTTATGGTATATGTTATTGTTTATGGCACTTGGGGCAGGTGGAAAAAATTCCACAC 128 8 TATTTTAGCACTGTTTTGTTTTATGGTATATTTTTATTGGCTACTTATTGTTTAGGAACACGTGGGGCTAGGGGAAGAAAAATTCCACAGC 128 7 TATTTTAGCACTGTTTTGTTTTATGGTATATTTTTATTGGCTACTTTATTGTTTAGGAACACTGGGGCTAGGGCAAGTGGAAAAAATTCCACAGC 128 8 TATTTTAGCACTGTTTTTTTTTATGGTATATTTTTATTGGCTACTTTATTGTTTAGGAACACTGGGGCTAGGGCAAGTGGAAAAAATTCCACAGC 128 8 TATTTTAGCACTGTTTTTTTTTATGGTATATTTTTATTGGCTACTTTATTGTTTAGGAA 7 TATTTTAGCACCTAGGACACACTGGGGCTAGGGCAAAAAAATTCCACAGC 128 8 TATTTTAGCACCTTTTTTTTTTTATGGTATATTTTTTTTT	Query Match Best Local Matches 66	ORIGIN	FEATURES	RESULT 8 BX095713 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	Qy 94 Db 12 Qy 100 Db 6	рь 24 Qy 88 рь 18
	55.8%; Score 665; DB 13; Length 765; Similarity 99.0%; Pred. No. 1.7e-83; 8; Conservative 0; Mismatches 7; Indels 0; Gaps	odified served by week year stores of the N interactions of the N interactions and the served by the	Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAGD998081942. RZPDLIB; I.M.A.G.E. cDNA Clone Collection; Human UniqueeSet - RZPD3 (RZPDLIB No.972) http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq Contact RZPD (clone@rzpd.de) for further information. Seq M13x, Primer sequence: TTTCACACAGGAAACAGCTATGAC. Locarion/Qualifiers 1. 765	765 bp mRNA linear EST 04-FEB-2 95713 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone N595713 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone N595713 1 GI:27842493 1 Spiens (human) 10 sapiens (human) 10 sapiens 11 Sutheria; Primates; Craniata; Vertebrata; Euteleostomi 12 mania; Eutheria; Primates; Catarrhini; Hominidae; Homo. 12 (bases 1 to 765) 12 to 765) 13 coares to 765) 14 heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., 18 lelof, U., Schneider, D. and Korn, B. 18 lalof, U., Schneider, D. and Korn, B. 18 lalof, U., Schneider, D. and Korn, B. 18 lalof, U., Schneider, D. and Korn, B. 19 Deutsches Ressourcenzentrum fuer Genomforschung GmbH	5 TTTTTTAGCACTGTTTTTGTTTTAATGGTATATTTTATTGGCTACTTTATTGTTTAGGA	

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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ORGANISM
                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                RESULT 9
BQ884216
LOCUS
DEFINITION
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 892)

1 (bases 1 to 892)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

LUppublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
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892 bp mRNA linear EST 16-AUG
AGENCOURT 8681949 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6197459 5', mRNA sequence.
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BQ884216.1 GI:22276224
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Best Local Similarity 95.6%;
Matches 741; Conservative
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                                                                                         AGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACGTCTC
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                                                                                                                                                                                                                                       GTGTGGGTGGGTCCGTTGGTTCCCCAAGATACTTTTAGGTGGTATGGGGGCCTGCATTAAGT
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Location/Qualifiers
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/note="vector: pcmV-SpORT6" (Life Technologies); Site_1:
/note="vector: pcmV-SpORT6" (Life Technologies); Site_1:
/note="vector: pcmV-SpORT6" (Life Technologies); Site_2: Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCACGCGTCCG-3' and
5'-GACTACTTCTAGATCGCGACGGCGCCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
Technologies."
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/dev_stage="adult, 70 yr"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6197459"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCMN159 row: j column: 07
High quality sequence stop: 712.
Location/Qualifiers
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1 (bases 1 to 714)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
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/tissue_type="epithelioid carcinoma cell line"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
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/clone lib="NIH MGC 42"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
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/site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5; adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 1.5e-81;
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1 (bases 1 to 713)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1855 row: d column: 05 High quality sequence stop: 709.
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/mol type="mRNA"
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/clone="MAGB:5091412"
/clone="type="epithelioid carcinoma cell line"
/tissue_type="epithelioid carcinoma cell line"
/tab_host="DH10B (phage-resistant)"
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/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EGORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Lir Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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JOURNAL
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Best Local Similarity
Matches 715; Conserv
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E 1 (bases 1 to 1104)

E National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Plate: LLCM1244 row: j column:
High quality sequence stop: 636.
                               CTCCATCCTGCTCCTCCTCCTGCTCATGATGCTTGGTGTTCGTGGCCTCCTCCTGGTTGG
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/mol type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAG:4550896"
/tissue_type="large cell carcinoma"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 18"
/clone lib="NIH MGC 18"
/clone lib="NIH MGC 18"
/clone corn(Xhol sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CNA synthesis ki (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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0; Mismatches 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Max-Planck-Institute for evolutionary Anthropology
Deutscher Platz 6, 04103 Leipzig, Germany
Tel: +49-(0)-341-3550 500
Fax: +49-(0)-341-3550 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. (2003) In press
Contact: Paabo S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CB296571 566 bp mRNA linear EST 28-12B22027_rev_1_B02_r_025.ab1 Chimpanzee brain library Koostroglodytes cDNA clone 12B22027_rev_1_B02_r_025.ab1 5', mRNA linear EST 28-12B22027_rev_1_B02_r_025.ab1 5', mRNA linear EST 28-12B220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evolutionary Genetics Max-Planck-Institute
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Pan troglodytes
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             il: paabo@eva.mpg.de
primer: Ml3 reverse.
                                                                     /lab_host="Epicurian Coli (TM) XL-10-Gold" / Clone lib="Chimpanzee brain library Koos" / Clone lib-EChimpanzee brain library Koos" / Clone library was prepared using the SMART cDNA library construction Kit (Clontech), doing only primer extension, but not PCR amplification of the cDNA. The only deviation from the published protocoll was that we cloned the cDNA into a plasmid Vector."
                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pan troglodytes"
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                                                                                                                                                                                                                                                                                                /tissue_type="brain, presumably cortex"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
Score
541.6;
DB
14;
Length
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	2138 617-495-1812 617-495-8557	
0	Williams,T., Jackson Endocrine Pancreas (Unpublished (2000) Other_ESTs: ir66f05. Contact: Douglas Mel Endocrine Pancreas (Harvard University, Dept of Molecular an	TITLE JOURNAL COMMENT
•	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 541) 1 (bases 1 to 541) Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylle, T., Marrin, J., Blistain, Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.	REFERENCI AUTHOR
••	 CA942743.1 GI:27431223 EST. Homo sapiens (human) Homo sapiens (buman) Homo sapiens Bukarvota: Metazoa: Chordata: Craniata: 	ACCESSION VERSION KEYWORDS SOURCE ORGANISM
2002	(C CA942743 541 bp mRNA linear EST 30-DEC- DN 1766f05.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6607449 3',	RESULT 14 CA942743/c LOCUS DEFINITION
	541 TAGGGGTGGGTTTGTTGA 558 - - - - - - -	P 64
40	CCTGGTGTCCCACCTGAGTCA(CTGGTGTCCCACCTGAGTCA(P 9
480 488	421 GCCGGTGACCTCCATCCTGCTCCTCCTCCTGATGATGCTTGGTGTTCGTGGCCTCCT 4	pb Qy
420 428	361 CAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGA 4	dg VQ
68	301 CCCCCGCCAGCAGCAGGCAGGCAGGCTGGGTGGGTGCTCAGTCCCCCTTCAATGACCT 3	₽ Q
80	241 TAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCCCCCAGGGGGTCCTGG 3	B 8
48	181 TGGGGAAATCGTGCAGGACGACGACGCCCCGAGTGAGGACCACTACCCAGCCACCAAGAGG 2	g Qy
180 188	121 TTCTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAA 1	P 8
120 128	61 CAGCATCTACTCAGCGTGGGTCACCTCTGTGAACATCACTGACTG	A A
80 0	1 AAACGGCCTGGAGGCCGCGGGAGTGGACGCCGCGAGGCCGGAGTCGCGCCTGCAGACA 6	당 왕
0;	Local Similarity 98.0%; Pred. No. 3.3e-66; hes 547; Conservative 0; Mismatches 11; Indels 0; Gaps	Best Loc Matches

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Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 455.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 45.0%;
Similarity 99.4%;
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIGIGITITCCCCTITGIGITAAGCGTGAGGCAGAGGGAGACGTTAGICCAGCAITTCCAA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGTGTTTTCCCCTTTGTGTTAAGCGTGAGGCAGAGGGGAGACGTTAGTCCAGCATTTCCAA
                                                                                                            AGCACIGITTITIGITTIAAIGGTAIAITTTTIATIGGCTACITTAITIGITTIAGGACAAGIG 1010
                                                                                                                                                                                                                                                        GAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACGTCT
                                                                                                                                                                                                                                                                                 GAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACGTCT
                                                                                                                                                                                                                                                                                                                                      TGGCACAAAATCAGAGCAAGAAAGCGATGCCCTTCCCAATTCTCTCAATCCTTTTATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTGTGGGTTGGGTTGGTTCCCCGAGATACTTTTAGGTGGTATGGGGGCCTGCATTAAG 770
GTAGTGGCATTCTATTTATTGTGACCTTTTCAATAAATAGATTTAAGTAAAAATGAAAAA 2
                                                                                    AGCACTGTTTTTGTTTTAATGGTATATTTTTATTGGCTACTTTATTGTTTTAGGACAAGTG
                                                                                                                                                                      CCTCTGCCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTTTTT 122
                                                                                                                                                                                          CCTCTGCCTAGGGACAGGACTTGGGCTTAGGGCAGGTGGAAAAAAATTCCAGACTTTTTT 950
                                                                                                                                                                                                                                                                                                                                                                                                                          AGTGTGGGTGGGTCCGTTGGTTCCCAAGATACTTTTAGGTGGTATGGGGCCTGCATTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: Noti; Site_2: XhOI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~lkb. 5' XhOI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Mashington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@alngate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:6607449"
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/clone_lib="HR85 islet"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'mol_type="mRNA"
'db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 536.2; DB 14; Length 541; Pred. No. 1.9e-65; 0; Mismatches 3; Indels 0;
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RESULT 15

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QY 544	Query Match Best Local Matches 53	ORIGIN		•		FEATURES source		JOURNAL MEDLINE PUBMED COMMENT	REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	BU733254/c LOCUS DEFINITION
4 GGGTGGGTTTGTTGAGAGGGACTTGCTGGGCCTTGGTCTGAGAGCAGGCATATTTGGAGG 603	<pre>ch 44.5%; Score 530.4; DB 13; Length 533; l Similarity 99.6%; Pred. No. 1.2e-64; 531; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</pre>	TAG_TISSUE=RPE and Chorold TAG_LIB=UI-E-CI1 TAG_SEQ=ACCTA"	rr~c ∙ parm	/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-CII is a normalized CDNA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I	o sapiens" A" 11-afs-m-18-0-UI" RPE and Choroid" ult " 08 (Life Technologies) (T1 phage re-		of Iowa of Iowa of Iowa food, 4156 MEBRF, Iowa City, IA 522 back second second second second second second second ry preparation: Dr. M. Bento Soares, Ury preparation: Dr. M. Bento Soares, Uring by: Dr. M. Bento Soares, Universibution: Researchers may obtain clon my resgen.com). second s	Genome Res. 6 (9), 791-806 (1996) 97044477 8889548 Contacts Soares, MB Contacts Isbaratory for Computational Genomics	Eutheria; Primates; Catarrhini 1 to 533) F., Lennon,G. and Soares,M.B.		533 bp mRNA linear EST 09-OCT-2002 UI-E-CI1-afs-m-18-0-UI.s1 UI-E-CI1 Homo sapiens cDNA clone UI-E-CI1-afs-m-18-0-UI 3', mRNA sequence.

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                   TITTAATGGTATATTTTTATTGGCTACTTTATTGTTTAGGACAAGTGGTAGTGGCAITCT 1023
                                                             CTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACGTCTCCTCTGCCTAGGG '903
                                                                                                       CCGTTGGTTCCCGAGATACTTTTAGGTGGTATGGGGCCTGCATTAAGTGGCACAAAATCA 783
                                                                                                                            TIGTGITAAGCGTGAGGCAGAGGGAGACGITAGTCCAGCATTTCCAAAGIGTGGGTGGGT 723
                                                                                                                                                 AGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTTTTTAGCACTGTTTTTG 963
                                                                                                                                                  414
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Search completed: August 22, 2004, 03:29:18 Job time : 3005 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Title: Perfect score: Sequence: Run on: US-10-001-885-31 1192 1 aaaccgcctggagc August 22, 2004, 00:20:26; Search time 117 Seconds (without alignments) 5653.859 Million cell updates/sec aaaccgcctggagccgccgg.....gaagaggacacacggaaccc 1192

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters:

1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Score	% Query Match	Length	BB	SUMMARIES	Description
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N	473	9		4.	US-09-621-976-864	e 864, 1
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7	45.6		664	4.	US-09-904-615-66	66
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10	45.2		2485	4		e 9,
11	45.2		3138	Н	07-	e 4,
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14	44.8		2381	_	US-08-021-608D-9	e 9,
15	44.8		2381	_	US-08-726-160-9	e 9,
16	44.8	3.8	2381	σ	PCT-US94-01782-9	9
17	44.8		2384	щ	US-08-021-608D-1	e 1,
18	44.8		2384	Ь	US-08-726-160-1	۲,
19	٠		2384	ຫ	PCT-US94-01782-1	,1
20	44.6	3.7	1466	4.	US-08-984-919A-10	Sequence 10, Appl
c 21	44.6		1466	4	US-08-984-919A-12	12
22	44.6		1472	W	US-08-781-420-10	e 10,
c 23	44.6		1472	ω	-781	12
24	44.6		1472	4	08-874	10,
c 25	44.6		1472	4,	-08-874	12,
26	44.6		1472	4.	US-09-006-595A-10	
c 27	44.6	3.7	1472	4.	US-09-006-595A-12	12,

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ω	4.	4	4	4	4	ω	ω	4,	4.	4	4	4	N	4	4	4	4
US-08-906-769-144	US-09-904-615-59	US-09-904-615-59	US-09-621-976-7782	US-09-621-976-7748	US-09-004-729-66	US-08-749-699-66	US-09-004-731-66	US-09-713-550-33	US-09-640-173-33	US-09-149-476-112	US-09-800-729-67	US-09-328-475C-236	US-08-070-301-2	US-08-874-102-48	US-08-874-102-46	US-08-984-919A-48	US-08-984-919A-46
	Sequence 59, Appl	Sequence 59, Appl	Sequence 7782, Ap	Sequence 7748, Ap	Sequence 66, Appl	Sequence 66, Appl	Sequence 66, Appl		33,	٠.	Sequence 67, Appl	Sequence 236, App	Sequence 2, Appli	Sequence 48, Appl	•	Sequence 48, Appl	Sequence 46, Appl

ALIGNMENTS

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DATE: 1997-05-23	NUMBER: 6	: 1997-05-23	NUMBER: 60	DATE: 1997-05-23	BER: 60	: 1997-05-23	ER: 6	: 1997-05-2	NUMBER: 6	: 1997-05-23	NUMBER: 60	: 1997-05-23	NUMBER: 60	: 1997-05-23	NUMBER: 60/047	4	. HUS - 60/047 FD	NUMBER: 6	: 1997-05-23	NUMBER: 60	: 1997-05-23	NUMBER: 60	: 1997-03-07	NUMBER: 6	: 1997-03-07	NUMBER: 60	DATE: 1997-03-07	WTWBEB: 60/040 33	NUMBER:	: 1997-03-07	NUMBER:	: 1997-03-07	NUMBER:	. 1997-03	: 1998-03-06	NUMBER: F	: 1998-09-08	TION NUMBER: US/09/149,476	102P1		er.	3 0	ication US/09149476		

ER AP	APPLICATION NUMBER: FILING DATE: 1997-0	60/047, 5-23		APPLICATION NUMBER
ER AP			·. ·.	EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,911
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י על ני	PPLICATION 1	NUMBER: 6	. ~. ~	FILING DATE: 1997-08-22
	PPLICATION I	1997-05-		APPLICATION NUMBER: 60/056
	APPLICATION N		~. ~.	1997-08-22
	PPLICATION 1	z	~ ~.	APPLICATION NUMBER: FILING DATE: 1997-0
	APPLICATION NUMBER:	60	~- ~-	FILING DATE: 1997-0
ER FI	FILING DATE: 1997-0 APPLICATION NUMBER:	: 1997-05-23 NUMBER: 60/047,632		FILING DATE: 1997-08-22
ER FI	PPLICATION :	23 0/047,	·· ··	APPLICATION NUMBER: 60/056 FILING DATE: 1997-08-22
	FILING DATE: 1997-05-	> N (. ~	ż
	FILING DATE: 1997-0	1997-04-11		APPLICATION N
BR AP	APPLICATION DATE:	APPLICATION NUMBER: 60/043,568		FILING DATE: APPLICATION N
	APPLICATION N			FILING DATE:
	PPLICATION NUMBER: 60		·	FILING DATE:
ER AP	PLICATION	EPELICATION NUMBER: 60/043,311		FILING DATE
3 ⊅ 14	PELICATION P	PPLICATION UNMBER: 60/043,671		EARLIER AFFILENTION NUMBER: 00/04/,500 EARLIER FILING DATE: 1997-05-23 EXELIER ADDITONTION NUMBER: 60/047 500
g Do n	PPLICATION NUMBER: 60	NUMBER: 60/043,674	. ~. •	·
g (** **	PPLICATION NUMBER: 60	NUMBER 60/043,669		FILING DATE:
ל וסל ו	PPLICATION I			FILING DATE: 1997-05-23
ER AP	PPLICATION 1		. ~. ~	EARLIER REFERENCE MONDEN. 00/04/1000 EARLIER FILING DATE: 1997-05-23 EARLIER ADDITION WITHDED. 60/047 614
	PPLICATION 1			FILING DATE:
70 X	APPLICATION N		٠	FILING DATE:
	APPLICATION 1	22	~. ~.	FILING DATE: 1997-04-11
ER FI	PPLICATION :	FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056,886	~. ~ .	60/047, 5-23
ER FI	FILING DATE: 1997-0	1997-08-22 NIMBER: 60/056-877	~.	EARLIER APPLICATION NUMBER: 60/043,670 EARLIER FILING DATE: 1997-04-11
	ILING DATE:			APPLICATION N
	FILING DATE: 1997-0	1997-08-22		APPLICATION NUMBER: 6
	ILING DATE:	FILING DATE: 1997-08-22	٠. ٠.	APPLICATION NUMBER: 6
ER AP	APPLICATION N FILING DATE:	APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22		EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,881
ER AP	APPLICATION :	APPLICATION NUMBER: 60/056,878	·. ·.	EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,909
	PLICATION		. ~	FILING DATE:
	APPLICATION N		٠. ٠.	FILING DATE: 1997-08-22
	PPLICATION N		٠. ٠.	FILING DATE: 1997-08-22
	APPLICATION NUMBER: 60	NUMBER: 60/056,637	·- ·-	1997-08-22
ER AP	APPLICATION :	NUMBER: 60/056,903	٠. ٠.	FILING DATE: 1997-08-22
er ei	PPLICATION	1997-08-22 NUMBER: 60/056,888	~. ~.	NUMBER:
ומי ע		1997-08-22 NIMHER - 60/056 879	~.	APPLICATION NU
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EARLIER RAPPLICATION NUMBER: 60/057,669
FILLING DATE: 1997-09-05
RAPPLICATION NUMBER: 60/049,610
FILING DATE: 1997-06-13
RAPPLICATION NUMBER: 60/061,060
FILING DATE: 1997-10-02 286 181 121 166 61 46 CAAGCCTCCCTCAATTTCTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAAGGATGGT Conservative 84.9%; ٥, Score 1012; DB 4; Pred. No. 1.2e-263; 0; Mismatches 5;

Length 1049; Indels

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CTTTTTTAGCACTGTTTTTGTTTTAATGGTATATTTTTATTGGCTACTTTATTGTTTAGG

1063

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Gaps

105

165 60

301 346 421 361 406 586 481 526 466 CAAGCCTCCCTCAATTTCTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGT CCAGCCACCAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCC GCGGATCTTGGCCAATGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACCACTAC GCGGATCTTGGCCAATGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACCACTAC ACCTCTGAGGGCTGATAGGGGTGGGTTTGTTGAGAGGGACTTGCTGGGCCTTGGTGAG rerrectedecerected recent description of the content of the conten TGTTCGTGGCCTCCTCCTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTG CAACCATGCTGTGGAGCCGGTGACCTCCATCCTGCTCCTCTTCCTGCTCATGATGCTTGG CCCCTTCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCATCTCGG CCCCTTCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGGAGTGGCATCTCGG CCCAGGGGGTCCTGGCCCCGCCAGCAGCAGGCAGGTGCCAGGCTGGGTGCTCAGTC CCCAGGGGTCCTGGCCCCCGCCAGCAGCAGGCAGGCTGCCAGGCTGCGGTGCTCAGTC ACCTCTGAGGGCTGATAGGGGTGGGTTTGTTGAGAGGGACTTGCTGGGCCTTGGTGAG 465 405 345 120 645 540 585 480 525 420 360 300 240 285 180 225

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APPLICANT: Johns Milne Edwards, J.B.
APPLICANT: Johert, S.
TITLE OF INVENTION: ESTs and Encoded Human P.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILLING DATE: 2000-07-21
NUMBER OF SEO ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 864
LENGTH: 483
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 171..482
US-09-621-976-864 RESULT 2
US-09-621-976-864
; Sequence 864, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION: S 밁 S Ś 8 吊 Ś Ś 닭 Ś B Ş 밁 S 밁 S 片 片 Query Match Best Local S Matches 473 1021 473; 181 131 431 421 371 361 311 301 251 241 191 121 71 61 11 μ. Similarity AAACCGCCTGGAGCCGCGGAGTGGACGCCGCCGAGGCCCGGAGTCGCGCCTGCAGACA AAACCGCCTGGAGCCGCCGGAGTGGACGCCGCCGAGGCCCGGAGTCGCGCCTGCAGACA AAAAAAAAAAAA **ААААААААААА** 1077 TTCTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAA GCCGGTGACCTCCATCCTGCTCCTCCTGCTCATGATGCTTGGTGTTCGTG CAACCGGCAGCTGGTGAACATGGGCTTTCCGCCAGTGGCATCTCGGCAACCATGCTGGGA CAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGA CCCCGCCAGCAGCAGGCAGGTGCCAGGCTGGTGCTCAGTCCCCTTCAATGACCT TAGCATICCTCGACAGAGCTICTTCAATAGGGGCCATGGTGCTCCCCCCAGGGGGGTCCTGG TGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACCACTACCCAGCCACCAAGAGG TGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACCACCACCACCAGCCACCAAGAGG TTCTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAA eccesia de contra de la contra del la contra della contra 39.7%; Score 473; DB 4; I ilarity 100.0%; Pred. No. 3.5e-118; Conservative 0; Mismatches 0; and Encoded Human Length 483 0 473 483 1020 180 130 70 420 360 310 240 190

RESULT 3 US-09-621-976-3064

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Sequence 3064, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3064
LENGTH: 519
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; Sequence 17202, Application US/09621976

; Patent No. 6639063
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; NAME/KEY: CDS
; LOCATION: 93..431
US-09-621-976-3064
                                                                                                            GENERAL INFORMATION:
APPLICANT: Dumas milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human
FILE REFERENCE: GENSET.054PR2
              NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 17202
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                                                                              CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
TYPE: DNA
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCCTGGCCCCGCCAGCAGCAGCAGGCAGGTGCMAGGCTGGGTGCTGCTCAGTCCCCCTTCA
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Pred. No. 3.2e-96;
1; Mismatches 3
                                                                                                                                 Proteins
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APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Didier RP
APPLICANT: Thomas, Didier RP
APPLICANT: Jepson, Ian
ITITLE OF INVENTION: Promoters
FILE REFERENCE: PPD 50108
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT FILLING DATE: 1997-03-22
EARLIER APPLICATION NUMBER: PCT/GB97/00729
EARLIER RILLING DATE: 1997-03-18
EARLIER FILLING DATE: 1997-03-18
EARLIER FILLING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 63
LENGTH: 1441
TYPE: DNA
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US-08-821-994-63
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GENERAL INFORMATION:
                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 82; Conserv
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Best Local
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                                                                AAAAAAAAAAAAAAAAAA 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCCCCCCAGCAGCAGGCAGGTGCCAGGCTGGG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARRYSGSMKGRARCCGCCKGGAGYSGMCKSSRSYGRRSSCCGSMGWSGCSCSKRSWSRCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08821994A
                                                                                                                                                                                                                                4.0%; ilarity 58.6%; Conservative
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                                                                                                                                                                                                                              Score 47.2; DB 3;
Pred. No. 0.0076;
0; Mismatches 58;
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TICTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAA 180
TGTTGGTCAATATCATTCATTCAAAGAATATTTGCTTTGGCTTGATTATGTATTAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTAGCACTGTTTTGTTTTAATGGTATATTTTTATTGGCTACTTTATTGTTTAGGAC 1005
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           Sequence 66, Application US/09904615
Patent No. 6586325
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PRO322P1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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CURRENT APPLICATION NUMBER: US/09/904,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMAT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Quine, Jonathan A.
REGISTRATION NUMBER: P-41,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: -
LOCATION: 1..1971
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UGA:
COUNTRY: UGA:
TTD: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Improved Promoters for Enhancing TITLE OF INVENTION: Productivity NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/892,770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 15-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                         1926 АТGAAAGTGATAAAAAAAAAAAAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                               1866 CCCGTCTTATTTACGTATGTCTGATAGAGATTATATTCACTCTAGTATCGTAACTTGGAG 1925
                                                                                                                                                                                                                                                                                                                                                           1806 AGATGAATAAATGCCTAAATAAAATTGCCACTTTACCTTTTCAAATGAAATTTATTATT
                                                                                                                                                                                                                                                                                                                     925 AGGTGGAAAAATTCCAGACTTTTTTAGCACTGTTTTTGTTTTAATGGTATATTTTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                     89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 3.8%;
Similarity 55.3%;
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Pautot, Veronique
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aminopeptidase 2 (LapA2) cDNA"
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GRGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (31)
GOTHER INFORMATION: n equals a,t,g, or
NAME/KEY: SITE
LOCATION: (63)
GOTHER INFORMATION: n equals a,t,g, or
US-09-904-615-66
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                                                                                                                               US-09-293-322C-8
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                                                                                                                                                                                                                                   SOFTWARE: Pate
SEQ ID NO 8
LENGTH: 2409
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pallas, David C
APPLICANT: Du, Xianxing
TITLE OF INVENTION: Coding Sequence for Protein Phosphata;
Patent No. 6232110
TITLE OF INVENTION: Recombinant DNA Molecules and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 8, Application US/09293322C
Patent No. 6232110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                               Matches
                                                                                               Query Match
                                                                                                                                                                                                                                                                             FILE REFERENCE: 105-97
CURRENT APPLICATION NUMBER: US/09/293,322C
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: US 60/082,202
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 17
NUMBER OF SEQ ID NOS: 17
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NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/098,634
PRIOR FILING TION NUMBER: 60/098,634
                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2409)
OTHER INFORMATION: N is
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                                                                                                                                                                                                         ORGANISM: Mus musculus
                                                                                                                                                                                                                          TYPE: DNA
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                                                                                Local
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                               930 GAAAAATTCCAGACTTTTTAGCACTGTTTTTGTTTTAATGGTATATTTTTATTGGCTA 989
                                                                 67;
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                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                        PatentIn Ver. 2.0
     TTTGTTTCTTTGTTATTTÄTGATCTTGTTTAAAGAAAATAAATATCTCCCAACCTTTAAA 2353
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                                                               Conservative
                                                                             3.8%;
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Pred. No. 0.013;
0; Mismatches 69;
                                                               Score 45.4; DB Pred. No. 0.031; 0; Mismatches
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                                                                                          DB 3;
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                                                                                              Length 2409;
                                                               Indels
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Sequence 9, Application US/09889463A

Patent No. 6680185

GENEERI INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Falco, Saverio C.

APPLICANT: Miao, Guo-Hua

TITLE OF INVENTION: Plant Polyphenol Oxidase Homologs

FILE REFERENCE: BB1330

CURRENT APPLICATION NUMBER: US/09/889,463A

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 60/119,590

PRIOR FILING DATE: 1999-02-10

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Microsoft Office 97

SEQ ID NO 9

LENGTH: 2485
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US-09-889-463A-9
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US-09-839-497A-8
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Patent No. 6528295
GENERAL INFORMATION:
APPLICANT: Pallas, David C.
APPLICANT: Du, Xianxing
TITLE OF INVENTION: Coding Sequence for Protein Phosphatase Methylesterase,
Patent No. 6528295
TITLE OF INVENTION: Recombinant DNA Molecules and Methods
FILE REFERENCE: Docket No. 6528295 105-97A
CURRENT APPLICATION NUMBER: US/09/839,497A
CURRENT FILING DATE: 2001-04-20
CURRENT FILING DATE: 2001-04-20
CURRENT FILING DATE: 2001-04-20
CURRENT FILING DATE: 2001-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/082,202
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/293,322
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
SEQ ID NO 8
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 67; Conserv
                                               TYPE: DNA
ORGANISM: Glycine max
09-889-463A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(2409)
OTHER INFORMATION: N is A, T, G or C.
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ORGANISM: Mus musculus
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3.8%;
55 8%;
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Pred. No. 0.031;
0; Mismatches 36; Indels 0
Score 45.2; DB 4; Pred No. 0.036;
               Length 2485
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US-07-867-106-4
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                                                                                                                                                                                                              ; MOLECULE TYPE:
; ANTI-SENSE: NO
US-07-867-106-4
                                                                                                                                                                                                                                                                                                                 TELECOMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPAC: 215-568-3499
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3138 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/07867106 Patent No. 5389526 GENERAL INFORMATION:
                                                                                                                                             Matches
                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: One Libert
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                   TYPE: NUCLEIC ACID STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Feeney, Joanne Longo REGISTRATION NUMBER: 35,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
984 TGGCTACTITATGTTTAGGACAAGTGGTAGTGGCATTCTATTTATTGTGACCTTTTCAA 1043
                                                                      1912
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                                                                                           924 CAGGIGGAAAAAATTCCAGACTITTTTAGCACTGTTTTTGTTTTAATGGTATATTTTTAT 983
                                                                      USA
                                                                                                                                           3.8%;
ilarity 54.9%;
Conservative
                                                                                                                                                                                                                                                SS: single
circular
E: DNA (genomic)
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: RICE-0002
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Score 45.2; DB 1; Length 3138; Pred. No. 0.041; 0; Mismatches 73; Indels 0
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US-09-790-988-1
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APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
                                                                                                                        PRIOR FILING DATE: 1999-1
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-1
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-0
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                   atent No. 6579701
                                                                                                                                                                                                                 CURRENT FILLING TO NUMBER: 60/PRIOR APPLICATION NUMBER: 60/
                                                    PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Buchnera sp.
                                                                                                                                                                                                                                                                                            ILE REFERENCE:
                                                                                                                                                                                                                                                                                                             PPLICANT: EXELIXIS, INC.

ITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED IN CANCE

ITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 3.8%;
Local Similarity 58.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280385 AAAAAATATCAAAAAAA 280402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280265 TTTTÄTGÄTCTTCATATTTTÄTAAAATTTTTTTATTTTTATTTTTÄATTTTÄATTTTÄAT
APPLICATION NUMBER: 60/
                                                                                         APPLICATION NUMBER:
                                                                         FILING DATE:
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                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/738,946 FILING DATE: 2000-12-14
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                                                                       2000-02-29
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                                                                                                          2000-02-29
                                                                                                                                             2000-01-28
                                                                                                                                                                                                                                                       2000-12-14
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                                                                                                                             60/185,879
                     60/189,701
                                                      60/186,150
                                                                                         60/185,880
                                                                                                                                                                60/178,580
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RESULT 14
US-08-021-608D-9
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; ORGANISM: Drosophila melanogaster
US-09-738-946-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08021608D Patent No. 5580760
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Best Local
                                                                                                  TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 2381
                                                                                                                                                                                                                                                                                                     SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/0
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: STREET: STREET: NEW YORK
CITY: NEW YORK
CTATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                           TOPOLICE: CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LEVENS, DA
ORIGINAL SOURCE:
            HYPOTHETICAL: N
                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                              NAME: WILLIAM S. FEILER REGISTRATION NUMBER: 26
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                        STRANDEDNESS:
                                                                                       TYPE: Nucleic acid
                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3386 GGGCCCCTAAATGGTTGGGGTTTAAACC 3414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3266 TTTTATTTTTCCTÄÄTTTTGTATGTTCTGCAÄATAAATGTGÄCTCTTTAÄÄAÄÄAÄAAAAAAA 3325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1053 TTAAGTAAAAAAAAAAAAAAAAAAAAAAAAGCTGTGGGGGGTTACCCGGGGCCAAAGG 1112
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                                                           Unknown
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                                             CDNA
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C., AND AVIGAN, MARK I.
NOVEL FUSE BINDING
                                                                                                                                                                 758-4800
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Pred. No. 0.053;
0; Mismatches
                                                                                                                                                                                                 2026-4063
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; OTHER INFORMATION: 470 bp variable OTHER INFORMATION: region where R is A or G. US-08-021-608D-9
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Patent No. 5734016
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.8%;
Best Local Similarity 59.4%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/726,160
FILING DATE: 04-0CT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,608
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063US
REFERENCE/DOCKET NUMBER: 2026-4063US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -08-726-160-9
                                                             TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORIGINAL HUMAN
CELL LINE: HL60
                                                                                                                                                                                                                                                             TELEPHONE: (212) 758-48
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 2381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERPECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN
OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MORGAN & FINI
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2236 Trigigatataaargractititicaatgratactiticactiticcaaatgcctgttttgtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                            (212) 758-4800
470 bp variable region where R is A or G.
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Pred. No. 0.045;
0; Mismatches 52;
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2295 밁 밁 Ś 밁 Ş Ś US-08-726-160-9 Matches Query Match Best Local Similarity 2356 AAAAAAA 2363 1078 AAAAAAA 1085 2296 СТТТАСАНТАБАТGATATGAAACСТСАБББАБАБАБАБАББББББББББББББББББББ 2236 TTTGTGATATAAATGTACTTTTCAATGTATACTTTCACTTTCCAAATGCCTGTTTTGTG 2295 958 TITTIGITITAATGGTATATITTTATTGGCTACTTTATTGTTTAGGACAAGTGGTAGTGG 1017 76; Conservative 3.8%; 59.4%; Score 44.8; DB 1; Pred. No. 0.045; 0; Mismatches 52; DB 1; Length 2381; Indels 0; Gaps

Search completed: August 22, 2004, 03:31:26 Job time : 122 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Title: Perfect score: US-10-001-885-31 1192 August 22, 2004, 02:37:36; Search time 595 Seconds (without alignments) 9840.778 Million cell updates/sec 1 aaaccgcctggagccgccgg.....gaagaggacacacggaaccc 1192

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1:0

Searched: 3228839 seqs, 2456066551 residues

Total number of hits satisfying chosen parameters:

6457678

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database Published_Applications_NA:* Cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

(cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

(cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

(cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

(cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

(cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

(cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

(cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

(cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

(cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*

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(cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

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(cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

(cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

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(cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

(cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	a a		!	Result
13	110	8 7 6 5	4004	, t
75.6 75.6 71.2	363.2 112.4 112.4	1012 1012 432.8	1192 1061.4 1023.2 1012	Score
6.00		36.3 5.3	100.0 0.08 8.58 8.48	% Query Match
461 633 420	612 2940917 2940917	1049 1049 643 365	1192 1108 11052 1052	% Query Match Length
15 15	7 15	10 13	13	ממ
US-10-074-475-38 US-10-074-475-39 US-10-074-475-127	US-10-076-747-64 US-10-027-632-174763 US-10-027-632-174763	US-09-882-171-58 US-10-164-861-58 US-10-001-885-30 US-10-076-747-65	US-10-001-885-31 US-10-264-237-619 US-10-302-172-94 US-09-809-391-58	ID
Sequence 38, Appl Sequence 39, Appl Sequence 127, App	Sequence 64, Appl Sequence 174763, Sequence 174763,		Sequence 31, Appl Sequence 619, Appl Sequence 94, Appl Sequence 58, Appl	Description

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68,	29,		63,	40,	30,	6039	17, A	28	4	14	34,	Sequence 46, Appl	70	653	Sequence 92, Appl	88	27	41	60	84	40	e 23,	159	158	81	۳	e 6,	63,		0

ALIGNMENTS

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; LENGTH: 1192
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-885-31
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APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and
FILE REFERENCE: DEX-0279
CURRENT APPLICATION NUMBER: US/10/001,885
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,061
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,257
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin version 3.1
SEQ ID NO 31
FIRMORY 1100
                                                                                                                                                                         Query Match 100.0%; Score 1192; DB 13; Length 1192; Best Local Similarity 100.0%; Pred. No. 6.9e-309; Matches 1192; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
AAACCGCCTGGAGCCGCGGGAGTGGACGCCGCCGAGGCCCGGAGTCGCGCCTGCAGACA
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US-10-264-237-619
Sequence 61:, Application US/10264237
Publication No. US20040009491A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
APPLICANT: Birse et al.
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR APPLICATION NUMBER: US/025,515
PRIOR FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 619
LENGTH: 1108
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1101)...(1101)
OTHER INFORMATION: n equals a,t,g, or c
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                  TTGAGAGGGACTTGCTGGGCCTTGGTGTGAGAGCAGGCATATTTTGGAGGGGATCTGGTGG
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; GENERAL INFORMATION: ; APPLICANT: Ruben et al. ; TITLE OF INVENTION: 186 Human Secreted proteins	; GEN ; AI	Qy 76 GTGGGTCACCTCTGTGAACATCACTGACTGCAAGCCTCCATTTCTGGTGCAGCCCA 135
LT 4 809-391-58 quence 58, Application US/09809391 blication No. US20030049618A1	RESULT 4 US-09-80 ; Sequen ; Public	OY 16 GCCGGGAGTGGACGCCCGAGGCCCGGAGTCGCCTGCAGACACAGCATCTACTCAGC 75
100 CHILLENIAN MANAGATTA AGTA AAAAAAA 1052	. da	Query Match 85.8%; Score 1023.2; DB 13; Length 1052; Best Local Similarity 98.3%; Pred. No. 1.2e-263; Matches 1034; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
	P &	FEATURE: NAME/KEY: CDS LOCATION: (365) -10-302-172-94
01	B &	sapiens
856 AIGTTCCGATGCCTGTGGAAGACATGCCGACGTCTCCTC	Qy db	
796 GATGCCCTTCCCAATTCTCTCAATCCTTTATGCCGAGJ	Qy	PRIOR APPLICATION NUMBER: US 10/225,251 PRIOR PILING DATE: 2002-08-20 PRIOR PILING DATE: 2002-08-20 PRIOR PILING DATE: 2002-08-05 PRIOR PILING DATE: 2002-08-05
736 GAGATACTTTTAGGTGGTATGGGGCCTGCATTAAGTGGG 	D Qy	IVENTION: Polypeptides INCE: 803 1CNCP ILCATION NUMBER: US/10/302,172 INC DATE: 2002-11-21
676 TGAGGCAGAGGGAGACGTTAGTCCAGCATTTCCAAAGTX	Db Qy	; GENESONI INFORMATION: ; APPLICANT: Tang, Y. Tom ; APPLICANT: Xue, Aidong J. ; APPLICANT: Drmanac, Radoje T. ; APPLICANT: Drmanac, Radoje T. ; TITLE OF INVERNITON: No. U8200A0053250Alel Arginine-rich Protein-like Nucleic Acids an
616 GCCTTGAAGGTATGATCAGAGAGGGGACCACAGGTGTGT 	D 97	RESULT 3 US-10-302-172-94 US-10-302-172-94 ; Sequence 94, Application US/10302172 ; Publication No. US20040053250A1 ; Publication No. US20040053250A1
556 TGAGAGGGACTTGCTGGGCCTTGGTGTGAGAGCAGGCA:	B &	Db 1021 CCTTTCAATAAATAGATTTAAGTAAAAAAAAAAAAAAAA
496 CTACCTGGTGTCCCACCTGAGTCAGCGGTGACCTCTGAC	B 8	Db 961 TATTTTTATTGGCTÄCTTATTGTTTATGGACAAGTGGTAGTGGCATTCTATTTATT
	B &	ACAAGTGGTAGTGGCATTCTATTTATTGTGA
361 GAACATGGGCTTTCCGGCAGTGGCATCTTCGGCAACCATGG 436 CCTGCTCCTCTTCCTGCTCATGATGGTTGGTGTTCGTGG	8 B	915 GGCT
301 GGCAGGTGCCAGGCTGGGTGCTGCTCAGTCCCCCTTCAG 376 GAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGG	, og B	QY 855 CATGTTCCGATGCCTGTGGAAGACATGCCGACGTCTCCTCTGCCTAGGGAGCAGGACTTG 914
	S S	Db 781 CGATGCCCTTCCCAATTCTCTCAATCCTTTATGCCGAGAAGATCTCAGCTGGATGCCAA 840
GARCGRCGCCCCGGAGIGAGGACCACTACCACTACCACTACCACTACCACTACCACTACCACTACT	\$ & B	735 CAGATACTITTAGGTGGTATGGGGCCTGCATTAAGTGGCACAAAATCAGAGCAAGAAG 79
GGACGACGCCCGAGTGAGGACCACTACCCAGCCA	. <i>Q</i> 8	
136 TCAGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTT	} &	601 TGCCTTGAAGGTATGATCAGAAGGGGACCACAGGTGTGTTTCCCCTTTGTGTTAAGC

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6 CTTTTCAATAAATAGATTTAAGTAAAAAAAA 1067 .	, 103	ð
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6 CTACCTGGTGTCCCACCTGAGTCAGCGGTGACCTCTGAGGGCTGATAGGGGTGGGT		Ş
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6 CCTGCTCCTCCTCCTCATGATGCTTGGTGTTCGTGGCCTCCTCCTGGTTGGCCTTGT 49	43	S
1 GAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGAGCCGGTGACCTCCAT 42	36	ם
6 GAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGAGCCGGTGACCTCCAT 43	37	8
GGCAGGTGCCAGGCTGGGTGCTCAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGT 36	30	닭
6 GGCAGGTGCCAGGCTGGGTGCTCAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGT 37	\vdash	ĮŞ
GCTTCTTCAATAGGGGCCATGGTGCTCCCCCAGGGGGTCCTGGCCCCCGCCAGCAGCA	24	밁
CAATAGGGGCCATGGTGCTCCCCCAGGGGGTCCTGGCCCCCGCCAGCAGCA	5	S
CAGCCACCAAGAGGTAGCATTCCTCGACA 2	18	문
ACGACCCCGAGTGAGGACCACTAC	19	S
CGGATCTTGGCCAATGGGGAAATCGTGCA 1	12	밁
ACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAATGGGGAAATCGTGCA 1	13	S

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; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT PILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
; SOCTWARE: Patentin Ver. 2.0
; SEQ ID NO 58
; LENGTH: 1049
; TYPE: DIA
; ORGANISM: Homo sapiens
US-09-809-391-58
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Best Local Similarity
Matches 1027; Conserv
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                                         Sequence 58, Application US/09882171
Publication No. US20030175858A1
GENERAL INFORMATION: 186 Human Secreted proteins
TITILE OF INVENTION: 186 Human Secreted proteins
FILL REFERENCE PRODEZ
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/899,391
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: 09/149,476
PRIOR APPLICATION NUMBER: 00/040,162
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PRIOR FILING DATE: 1997-05-23
PRIOR PRICING MUMBER: 60/047,492
PRIOR PRICING DATE: 1997-05-23
PRIOR PRILING DATE: 1997-06-23
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Best Local Similarity 99.3%;
Matches 1027; Conservative (
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Pred. No. 1.3e-260;
0; Mismatches 5;
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US-10-164-861-58
US-10-164-861-58
Sequence 58, Application US/10164861
Publication No. US20030225248A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITILE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 58
LENGTH: 1049
TYPE: DNA
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                                     ACCTCTGAGGGCTGAIAGGGGTGGGTTTGTTGAGAGAGGACTTGCTGGGCCCTTGGTGTGAG 585
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341 CAGTCCCCTTCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCAT 400	281 GCTCCCCAGGGGGTCCTGGCCCCGCCAGCAGCAGGCAGGC	221 ACTACCCAGCCACCAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGT 280	161 ATGGTGCGGATCTTGGCCAATGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACC 220	y Match 30.5%; Score 363.4; DB 15; Length 365; Local Similarity 99.7%; Pred. No. 6.5e-87; hes 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	CURRENT APPLICATION NUMBER: US/10/076,747 CURRENT FILING DATE: 2002-02-13 PRIOR APPLICATION NUMBER: 60/268,290 PRIOR FILING DATE: 2001-02-13 PRIOR APPLICATION NUMBER: 60/268,834 PRIOR FILING DATE: 2001-02-15 NUMBER OF SEQ ID NOS: 129 SOFTWARE: Patentin version 3.1 SEQ ID NO 65 LENGTH: 365 TYPE: DNA ORGANISM: Homo sapien US-10-076-747-65	Sequence 65, Application US/10076747 Publication No. US20030180726A1 GENERAL INFORMATION: APPLICANT: Salceda, Susana APPLICANT: Hu, Ping APPLICANT: Recipon, Herve APPLICANT: Karra, Kalpana APPLICANT: Karra, Kalpana APPLICANT: Liu, Chenghua APPLICANT: Liu, Chenghua APPLICANT: Liu, Chenghua APPLICANT: Liu, Chenghua APPLICANT: DEREPENCE: DESCRIPSITIONS and Methods Relating to Ovarian Specific Genes and P	5-747-65	GGTTCTCCCGCCCAATTCCCCCCAAATTTTTGACAAAATGAAGAGGACACACGGAACCC 643	1.33 CC. MINISTER MANAGEMENT AND THE TOTAL OF THE TOTAL O	1073 AAAAAAAAAAAAAAAAGCTGTGGGGGTTACCCCGGGGGCCAAAGGGGGGCCCCGGGGGGGAATGT 1132 	464 GTGGCATTCTATTATTGGTGACCTTTTCAATAAATAGATTTAAGCAAAAAAAA	14	955 CTGTTTTTGTTTTATGGTATATT-TTTATTGGCTACTTTATTGTTTAGGACAGTGGTA 1013 956 CTGTTTTGTTTTAATGGTATATT-TTTATTGGCTACTTTATTGTTATAGGACAAGTGGTA 463 404 TGTATTTTGTTTTAATGGTATATTCTATATTGGCTACTTTATTGTATATGGACAAGTGGTA 463	4 CCTAGGGAGCAGGACTTGGGCTAGGGCAGGTGGAAAAAATTCCAGACTTTTTTAGACAC 4	897 CCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTTTTTAGCA 954		837 ATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACGTCTCCTCTG 896

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APPLICANT: KATTA, Kalpana
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
ITILE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and FILE REFERENCE: DEX-0315
CURRENT APPLICATION NUMBER: US/10/076,747
CURRENT APPLICATION NUMBER: 60/268,290
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: 60/268,834
PRIOR APPLICATION NUMBER: 60/268,834
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOBER: 2001-03-15
SOFTWARE: Patentin version 3.1
LENGTH: 612
TYPE: DNA
ORGANISM: Homo sapien
US-10-076-747-64
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Best Local Similarity
Matches 456; Conserv
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APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
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87.7%; Pred. No. 1e-86;
tive 0; Mismatches 53;
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SOFTWARE: FASKSEQ for Windows Version 4.0
SEQ ID NO 174763
LENGTH: 2940917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.4%;
Best Local Similarity 66.5%;
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ORGANISM: Human
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NAME/KEY: misc_feature
LOCATION: (1)...(2940917)
OTHER INFORMATION: n = A,T,C or
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APPLICANT: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PRICING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PRIOR PRIOR DATE: 1999-09-28

PRIOR PRIOR PRIOR DATE: US 60/146,002
                                            Sequence 38, Application US/10074475
Publication No. US20030092898A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
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, NAME/KEY: misc_feature

, LOCATION: (1)...(2940917)

, OTHER INFORMATION: n = A,T,C or G

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US-10-027-632-174763/c
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LENGTH: 2940917
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SOFTWARE: FastSEQ for Windows Version 4.0
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Karra, Kalpana
Cafferkey, Robert
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 39
LENGTH: 633
TYPE: DNA
CRCANISM: Homo sapien
US-10-074-475-39
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US-10-074-475-39
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APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
FILE REFERENCE: DEX-0313
CURRENT APPLICATION NUMBER: US/10/074,475
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/268,292
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 295
SOFTWARE: Patentin version 3.1
SEQ ID NO 38
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                   Matches
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Best Local S
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APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
FILE REFERENCE DEX-0313
CURRENT APPLICATION NUMBER: US/10/074,475
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/268,292
PRIOR FILING DATE: 2001-02-13
RUMBER OF SEQ ID NOS: 295
RUMBER OF SEQ ID NOS: 295
RUMBER OF SEQ ID NOS: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
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TYPE: DNA
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1166 ACAAAA 1171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 GCTTTTTCCTTTTGTGGCTCAAAGGTAGCTGCATTTTAAAATATTTTGTGAAAATAAAAAAC 330
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                                    117;
                                                                                                        Similarity
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                                                                                 Conservative
                                                                                                        62.9%;
                                                                               Score 75.6; DB 15;
Pred. No. 1.5e-09;
0; Mismatches 69;
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RESULT 15
US-10-021-323-6568
(US-10-021-323-6568)
(Sequence 6568, Application US/10021323)
(Publication No. US20040123340A1)
(GENERAL INFORMATION:
(APPLICANT: Deikman, Jill
(APPLICANT: Feng, Paul C.C.
(APPLICANT: Ziegler, Todd E.
(APPLICANT: Ziegler, Todd E.
(APPLICANT: Ziegler, Todd E.
(APPLICANT: Dei INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
(TITLE OF INVENTION: Plants
(FILE REFERENCE: 38-21(52274)B
(CURRENT APPLICATION NUMBER: US/10/021,323)
(CURRENT FILING DATE: 2001-12-12
(PRIOR APPLICATION NUMBER: US 60/255, 619
(PRIOR APPLICATION NUMBER: US 60/255, 619
(PRIOR FILING DATE: 2000-12-14
(NUMBER OF SEQ ID NOS: 17880)
(SEQ ID NO 6568)
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US-10-074-475-127
; Sequence 127, Application US/10074475
; Publication No. US20030092898A1
; GENERAL INFORMATION:
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TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Compositions and Proteins
TITLE OF INVENTION: Genes and Proteins
CURRENT FINVENTION: Genes and Proteins
FILE REFERENCE: DEX-0313
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/268,292
PRIOR APPLICATION NUMBER: 60/268,292
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 295
SOFTWARE: PatentIn version 3.1
SEQ ID NO 127
TENGRAL 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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ORGANISM: Homo sapien
-10-074-475-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
APPLICANT: Karra, Kalpana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1055 AAGTAAAAAAAAAAAAAAAAAAAAAAAAAGCTGTGGGGGTTACCCGGGGCCAAAGGGG 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 GCCCCGGGGGCGAATTGGGTTCTCCCGGCCCACATTCCCCCAAAATATTGGCACA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCGGGGGAACCCGGGGCCCAGAGCGG
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Recipon, Herve
Karra, Kalpana
Cafferkey, Robert
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Search completed: August 22, 2004, 04:52:06 Job time : 605 secs
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                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                      FEATURE: UNBURE

LOCATION: (1)..(480)

OTHER INFORMATION: Unsure at all n locations

OTHER INFORMATION: Clone ID: LIB3828-008-Q1-N6-A12
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 480
TYPE: DNA
ORGANISM: Gossypium hirsutum
                                                                            1065 АЛАЛЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАССТGTGGGGGTTACCCGGGGCCAAAGGGGGGCCCCGGGG 1124
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                                                                                                                                      945 TTTTTTAGCACTGTTTTTTTTATTGGTATATTTTTTATTGGCTACTTTATTGTTTAGGA 1004
                                                                                                            62.2%;
                                                                                                                                                                                                                   Score 71.2; DB 17;
Pred. No. 1.9e-08;
0; Mismatches 68;
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GenCore version 5.1.6 Copyright (a) 1993 - 2004 Compugen Ltd.

Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Scoring table: Post-processing: Listing first 45 summaries Title: Perfect score: Run on: Total number of hits satisfying chosen parameters: Word size : Searched: OM nucleic - nucleic search, using sw model OLIGO_NUC Gapop 60.0 , Gapext 60.0 US-10-001-885-31 1192 1 aaaccgcctggagc August 22, 2004, 03:31:33; Search time 4687 Seconds (without alignments)
11023.020 Million cell updates/sec 3470272 seqs, 21671516995 residues 0 GenEmbl:* aaaccgcctggagccgccgg.....gaagaggacacacggaaccc 1192 ggboothing ggboothing ggboothing ggboothing ggboothing ggb em_mu:*
em_on:*
em_ov:*
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em_htgo_mus:*
em_htgo_other:* gb_ro:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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TITLE	AUTHORS	SOURCE	VERSION VERSION	RESULT 1 AX431088 LOCUS DEFINITI		45	4.4.	4, 4	C 41	. ω		c 36	w	ດ ພູພ ພູຊ	32	30	29		C 26	2 4	c 23	N) E	20		C 18	16	101 11 11	13	12	11	c i o		ე თ	Ω 5	J 4	ואי	1	Result No.
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methods relating to ovary	Salceda,S., Sun,Y., C	Chordata; Craniata; V Primates; Catarrhini;	065	1192 bp DNA ent WO0240535.	ALIGNMENTS	AC004707	AL663050	AL512503	AF326737	BC060865	BD069550	AR170130	AR170129	BC046243 AK130049	BC009221	AF379640 BC025044	BC062727	AC107741	BX571972	AC023979	BX004813	AY089465	BX571714 BX321879	AC119162	AC139357	AC040159	HUAC004514	AC019069	AX431087	BD110980	G22561	AX113082	AR413227	219	5031	013	ו סכ	ID
y specific genes and	afferkey,R. and	Vertebrata; Euteleostomi; i, Hominidae; Homo.		linear PAT 28-JUN-2002		Homo	Mou	AL512503 Human DNA	STIM	Omo	love	AR170130 Sequence	eque	BC046243 Homo sapi AK130049 Homo sapi	omo sapi	AF379640 Heliothis BC025044 Mus muscu	BC062727 Homo sapi	ine mui	ani	AC023979 Homo sapi	BX004813 Zebrafish	AY089465 Drosophil	BX371714 Danio rer BX321879 Danio rer	ACI19162 Mus muscu	u su	9 9	AC004514 Homo sapi	9 9	eque	AK41542/ Sequence BD110980 EST and e	G22561 human STS W	AX113082 Sequence	equence	omo :	AL450311 Human DNA	13587 Homo	AX431088 Sectionce	Description

661 CCTTTGTTAAGCGTGAGGCAGAGGGAGAGGGTAGTCCAGCATTTCCAAAGTGTGGGTG 721 GGTCCGTTGGTTCCCCGAGATACTTTTAGGTGGTATTGGGGCCTGCATTTAAGTGGACAAAA 721 GGTCCGTTGGTTCCCCGAGATACTTTTAGGTGGTATTGGGGCCTGCATTAAGTGGCACAAAA 721 GGTCCGTTGGTTCCCCAGATACTTTTAGGTGGTATGGGGCCTGCATTAAGTGGCACAAAA 721 GGTCCGTTGGTTCCCCAAATCTTTTAGGTGGTATGGGGCCTTTTATGCCGAGAAGAAAA 731 TCAGAAGCAAGAAAGCGATGCCCTTCCCCAATTCTCTCAATCCTTTTATGCCGAGAAGAATCT 781 TCAGAAGCAAGAAAGCGATGCCCTTCCCCAATTCTCTCAATCCTTTTATGCCGAGAAGAATCT 781 TCAGAAGCAAGAAAGCGATGCCCTTCCCCAATTCTCTCAATCCTTTTATGCCGAGAAGAATCT 781 TCAGAAGCAAGAAAGCGATGCCCTTCCCCAATTCTCTCAATCCTTTTATGCCGAGAAGAATCT 781 TCAGAAGCAAGAAAGCGATGCCCTTCCCCAATTCTCTCAATCCTTTTATGCCGAGAAGAATCT 781 TCAGAAGCAAGAAAGCGATGCCCTTCCCCAATTCTCTCAATCCTTTTATGCCGAGAAGAATCTTTTATGCCGAGAAGAATCTTTTATGCCGAGAAGAATCTTTTATGCCGAGAAGAATCTTTTATGCCGAGAAGAATCTTTTATGCCGAGAAGAATCTTTTATGCCGAGAAGAAGATCTTTTATGCCGAGAAGAATCTTTTATGCCGAGAAGAATCTTTTATGCCGAGAAGAATCTTTTATGCCGAGAAGAATCTTTTATGCCGAGAAGAAGATCTTTTATGCCGAGAAGAATCTTTTATGCCGAAGAAGAATCTTTTATGCCGAAGAAGAATCTTTTATGCCGAAGAAGAATCTTTTTTTT	CCTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGTGACCTCTGAGGGCTGA	TAGGATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCCCCCAGGGGGTCCTGG		roteins atent: WO 0240535-A 31 23-MAY-2002; location/Qualifiers 1. 1192 /organism="Homo sapiens" /mol_type="numassigned DNA" /db_xref="taxon:9606" 100.0%; Score 1192; DB 6; Length 1192; Similarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0; Gaps AAACCGCCTGGAGCCGCCGGGAGTCGACCGCCGCGGAGTCGCCGCAGACA
720 TITLE D 70URNAL G 780 REMARK N 780 COMMENT E 840 COMMENT T 900	TITLE JOURN PUBM REFEREN AUTHOI	300 SOURCE H 300 ORGANISM H 300 REFERENCE 1 360 REFERENCE 1 420 AUTHORS S 420 S 480 S	60 Qy 1141 120 Db 1141 120 RESULT 2 BC013587 180 LOCUS BCFINITION H 240 ACCESSION B 240 VERSION B	. Qy 901 Db 901 Qy 961 Db 961 DD 961 Qy 1021 O _j 1081 O _j 1081
irect Submission Livect McCollection (McCol), Cancer Genomics Office, National Cancer Genititute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, SA Livect McCollect URL: http://mgc.nci.nih.gov Livect McCollect McC	orley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., orley, K.C., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., ahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., anchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., ouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., ickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., utterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Uhnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. eneration and initial analysis of more than 15,000 full-length uman and mouse cDNA sequences roc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) (207932 (bases 1 to 1129)	MGC. Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. El (bases 1 to 1129) El (bases 1 to 1129) Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mallahy,S.J., Bounaratne,P.H., Richards,S., MCKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,	CGCCCCAATTCCCCCCAAATTTTTGACAAAATGAAGGACACACGGAACCC 1192	GGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTTTTTAGCACTGTTT 960

Ś 밁 Ś 밁 Ś 밁 δ 닭 Ś 멂 8 밁 Š 밁 Ś 문 FEATURES Query Match
Best Local Sim:
Matches 1083; gene Sdo source 121 482 421 422 361 362 301 302 241 242 181 GGGGAAATCGTGCAGGATGACGACCCCCGAGTGAGGACCACTACCCAGCCACCAAGAGGT 182 122 61 62 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 14 Row: i Column: 13
This; clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21687152
Location/Qualifiers Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M.; Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M. \vdash N h 86.7%; Similarity 99.9%; 83; Conservative CTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTGACCTCTGAGGGCTGAT CCGGTGACCTCCATCCTGCTCCTCCTCCTCCTCATGATGCTTGGTGTTCGTGGCCTCCTC ААССОВСАВСТВОТВААСАТОВОСТТТССВСАВТЕВСАТСТСВОСААССАТВСТВТВВАВ CCCCGCCAGCAGCAGGCAGGTGCCAGGCTGGGTGCTCAGTCCCCCTTCAATGACCTC AGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCCCCCAGGGGGGTCCTGGC AGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCCATGGTGCTCCCCCAGGGGGGTCCTGGC TCTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAAT TCTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAAT 181 AACCGCCTGGAGCCGCCGGAGTGGACGCCGCCGAGGCCCGGAGTCGCGCCTGCAGACAC AACCGCCTGGAGCCGCCGGAGATGGACGCCCGAGGCCCGGAGTCGCGCCTGCAGACAC CCGGTGACCTCCATCCTCCTCCTCCTCCTCCTCATGATGCTTGGTGTTCGTGGCCTCCTC AACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGAG CCCCGCCAGCAGCAGGCAGGTGCCAGGCTGCTGCTCAGTCCCCCTTCAATGACCTC /codon_start=1
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481

CTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTGACCTCTGAGGGCTGAT

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2	COMMENT	TITLE JOURNAL	REFERENCE AUTHORS	RESULT 3 ED191093 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Db	Ş	B 8	p &	g Q	p 8	ත් දි	B 8	р <i>Q</i>	р <i>Q</i>	Db Qy
PR 07-MAR-1997 US 60/040162,07-MAR-1997 US 60/04033 PR 07-MAR-1997 US 60/038621,07-MAR-1997 US 60/040161 PR 07-MAR-1997 US 60/040626,07-MAR-1997 US 60/04034 PR 07-MAR-1997 US 60/040336,07-MAR-1997 US 60/040334 PR 07-MAR-1997 US 60/040336,07-MAR-1997 US 60/040163 PR 11-APR-1997 US 60/043580,11-APR-1997 US 60/043568 PI STEVEN M RUBEN,CRAIG A ROSEN,CARRIE L FISCHER,DANIEL R SOPPET, PI KENNETH C CARTER,DANIEL P BEDNARIK,GREGORY A ENDRESS,GUO LIANG PI YU,JIAN NI, PI PING FENG,PAUL E YOUNG,JOHN M GREENE,ANN		186 human secreted protein patent: JP 2002510192-A 5 HUMAN GENOME SCIENCES INC		BD191093 1049 bp DNA linear PAT 17-UUL-2003 ON 186 human secreted proteins. N BD191093.1 GI:33000832 JF 2002510192-A/57. unidentified SM unidentified sm unidentified	1081 AAAA 1084	1082 AAAA 1085	1022 CTATTTATTGTGACCTTTTCAATAAATAGATTTAAGTAAAAAAAA	962 IGTTTTAATGGTAFATITTTATTGGCTACTTTATTGTTTAGGACAAGTGGTAGTGGCATT 1021 	902 GGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTTTTTAGCACTGTTTT 961 	842 AGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACGTCTCCTCTGCCTAG 901	782 CAGAGCAAGAAAGCGATGCCCTTCCCAATTCTCTCAATCCTTTTATGCCGAGAAGATCTC 841	722 GTCCGTTGGTTCCCGAGATACTTTTAGGTGGTATTGGGGCCTGCATTAAGTGGCACAAAAT 781 	662 CTTTGTGTTAAGCGTGAGGGAGAGGGAGACGTTAGTCCAGCATTTCCAAAGTGTGGGTGG	602 GGGGATCTGGTGGTGCCTTGAAGGTATGATCAGAGAGGGGACCACAGGTGTGTTTCCC 661	542 AGGGTGGGTTTGTTGAGAGGGACTTGCTGGGCCTTGGTGTGAGAGCAGGCATATTTGGA 601

	704 660 763	Qy 586 AGCAGGCATATTTGGAGGGATCTGGTGGTGCCTTGAAGGTATGATCAGAGAGGGGACCA 645	Qy 526 ACCTCTGAGGGCTGATAGGGGTTTGTTGAGAGGGACTTGCTGGGCCTTGGTGTGAG 585	Oy 466 TGTTCGTGGCCTCCTCCTGGTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTG 525	Qy 406 CAACCATGCTGTGGAGCCGGTGACCTCCTGCTCCTTCCTGCTCATGATGCTTGG 465	Qy 346 CCCCTTCAATCACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCATCTCCG 405		Qy 226 CCAGCCAACAAGAGGTAGCATTCCTCGACAGAGGTTCTTCAATAGGGGCCATGGTGCTCC 285 REFERENCE 1 (bases 1 to 165110)	X X	Sequence, AL450311 AL450311.11 GI:146269	Qy 46 TCGCGCCTGCAGACACACACATCACTCAGCGTGGGTCACCTCTGTGAACATCACTGACTG	Query Match 66.4%; Score 792; DB 6; Length 1049; Best Local Similarity 99.8%; Pred. No. 0; Matches 1032; Conservative 0; Mismatches 0; Indels 2; Gaps 2;	/organism="unidentified" Qy 1004 /mol_type="genomic_DNA" /mb_xref="taxon:32644" Db 961	The Article Property of the Ar	2,C12N5/10,C12N1/21,C07K14/47,C07K16/18,C12Q1/68, PC Qy 884 3,G01N33/68,A61K38/17 Db 841 Desc. Double.	JING SHAN HU, KIMBERLY A FLORENCE, HENRIK OLSEN, REINHARD ESBER, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI OLSEN, LAURIE A BREWER, LAURIE A BREWER	721 Db 721
sequence is the entire insert of clone RP11-343J3 The true end of clone RP11-249G2O is at 139955 in this sequence. The right end of clone RP11-404C6 is at 6588 in this sequence.	ger.ac.uk/HGP/Chr10 from the library RPCI-11.2 cc from For further details see ri.org/bacpac/home.htm	Lacadase can be round at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 wasping Group. Further information can be found at	tions are used to associate primary accession numerous table with their source databases: Em:, ENT; Tr; TREMBL; Wp:, WORMPEP; Information on the	30); an attempt was made to resolve all sequencing problems, s as compressions and repeats; all regions were covered by at le one plasmid subclone or more than one M13 subclone; and the assembly was confixmed by restriction digest. The following	less otherwi	where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found to the sequence submission to the overlapping clone, as we submit sequences with	CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 8, 2001 this sequence version replaced gi:14575291. During sequence assembly data is compared from overlapping clones	s 1 to 165110) ubmission d (12-JUL-2001) Sanger Centre, Hinxton, Cambrid	Homo sapiens (human) Homo sapiens Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	GI:146269	A segmence from clone RP11.143.13 on chromosome 10.	дадалада 1077 дадалада 1034	ACAAGTGGTAGTGGCATTCTATTTATTGTGACCTTTTCAATAAATA	CTTTTTAGCACTGTTTTGTTTTAATGGTAFATTTTTATTGGCTACTTTATTGTTTAGG	GACGTCTCCTCTGCCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGA 	TTATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCC	CATTAAGTGGCACAAAATCAGAGCAAGAAAGCGATGCCCTTCCCAATTCTCTCAATCCTT

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39. .19400
39. .19627
36. .19627
36. .19627
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38. .7917 of consensus"
38. .7917 of consensus" :3..13876
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6. .1602 77. .11372 "e="AluSx repeat: matches 1. .294 of consensus" 10. .11639 e="AluSx repeat: matches 1. .134 of consensus" 9. .20010 e="21 copi e="MER81 repeat: matches 2. .114 of consensus"
9. .18069
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                                                                                                                                                                                                                           /98. .45909
bte="LTR41 r
                                                                                                                                                                                             26. .46871
te="23 copies 2 mer gt 97% conserved"
                                                                                                                                                           te="AluSq repeat: matches 1.
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10. .45300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---"L2 repeat: matches 2097.
13. .23837
e="Aludb rerror"
                                          e="L1M4 repeat:
11. .54432
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                                                                                                              e="AluSx repeat: matches 1.
2.,52519
                                                                                                                                                                                                                                                                                                                        3. .44579
e="THELC repeat: matches 1. .371 of consensus"
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e="MITIJ repeat: matches 117. .413 of consensus"
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6. .41460
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3. .24850
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3. .24137
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|. .31156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dence=not_experimental
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                                                                                           ="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                 ="L2 repeat: matches 1448. .1779 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :="MIR repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ="AluSx repeat: matches 1. .292 of consensus"
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       ram repeat: matches 2.
.54629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uSx repeat: matches 1. .300 of consensus"
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                                                                                                                                                                                                                               repeat: matches 90. .192 of consensus"
                                                         matches 3865.
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CE Castle, A., Abraham, H., Allen, M., Anderson, S., Balchin, C., Barman, C., Lander R., Abraham, H., Allen, M., Anderson, S., Balchin, C., Barman, C., Barman, B., Watter, C., Castle, A., Begualarki, D., Backleg, C., Castle, A., Begualarki, C., Balchin, C., Barman, C., Castle, A., Begualarki, C., Backleg, C., Castle, A., Begualarki, C., Child, C
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1 (bases 1 to 173341)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 10, clone RP11-57E12

Unpublished
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AC021954.3 GI:7417809
ATG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
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RESULT 5 AC021954/c LOCUS

DEFINITION

AC021954 173341 bp DNA linear HTG 24-AUG-2002 Homo sapiens chromosome 10 clone RP11-57E12 map 10, WORKING DRAFT

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FEATURES
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/clone_lib="RPCI-11
                                                           /map="10"
                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Similarity 100.0%; Pi
69; Conservative 0;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human STS WI-12709, sequence tagged site.
                                                                                                                                                                                          Derived from dbEST (genbank accession H49529).
Location/Qualifiers
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STS; STS sequence; primer; sequence tagged
Homo sapiens (human)
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Unpublished (1995)
                                                                                                                                                                                                                                                                                                Buffer:
                                                                                                                                                                                                                                                                                                                                                                                                     Protocol:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitehead Institute/MIT Center for Genome Research; Physically
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KCl: 50 mM
Tris-HCL: 10 mM
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Primer: each 5 pM
dNTPs: each 4 nM
Tag Polymerase: 0.025 units/ul
Total Vol: 20 ul
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Annealing: 56 degrees (
Polymerization:
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                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/db_#431.2 cR from top of
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Sequence
AR415427
BD110980 EST and encoded human pr
BD110980
BD110980.1 GI:23205798
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Edwards, J. B.D. M., Jobert, S. and Giordano, J.-Y.
EST's and encoded human proteins
Patent: US 663963-A 3064 28-OCT-2003;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unclassified.
                                                                                                                                                                                                                                                       CAATGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACCACTACCCAGCCACCAAG
                                                                                                                                                                            AGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCCCCCAGGGG 293
                                                                                                                                                                                                                                                                                                                                        AATTTCTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGC 177
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/mol_type="genomic DNA"
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99.6%;
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CE 1 (bases 1 to 519)

Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.

EST and encoded human protein

Patent: JP 2002010789-A 3057 15-JAN-2002;

GENSET CORP

OS Homo sapiens (human)

PN JP 2002010789-A/3057

PD 15-JAN-2002

PP 07-AUG-2000 JP 2000280989

PF 07-AUG-2000 JP 2000280989

PF 07-AUG-2999 US 60/14/499

PF 07-AUG-1999 US 60/14/499

PI JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI

GIORDANO

C C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC

C12N1/21,

PC C12N15/00, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00

CC EST and encoded human protein

FH Key

TOGATIC (CINITIES)

1. CORTICO (CINITIES)

PR CDS

TOGATIC (CINITIES)

PR CDS

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                                                                                                                                                                                                                                                                                                     AX431087
Sequence 30 from Patent
AX431087
                                                        DIADEXUS INC
                                                                                                                 Compositions and
                                                                                                                                   Recipon, H., Liu, C., Salceda, S., Sun, Y., Macina, R.A.
                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                            Homo sapiens (human)
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                                                                          Patent: WO 0240535-A 30 23-MAY-2002;
                                                                                               proteins
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1. .643
/organism="Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Pred. No. 2.1e-101;
0; Mismatches 1;
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  sapiens"
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                                                                                                                                                                                                             Direct Submission

Direct Submission

Submitted (21-FEB-2002) Department of Genetics, Washington Submitted (21-FEB-2002) Department of Genetics, Missouri 63108, University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Jan 3, 2002 this sequence version replaced gi:16259101.

On Jan 3, 2002 this sequence Center

On Jan 3, 2002 this sequence Center

Thirarsity Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68584 bp DNA
Homo sapiens BAC clone RP11-259N19 from 2,
AC019069
AC019069.B GI:18042390
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 68584) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 68584)
                                                                                                               Center project name: H_NH0259N19
                                                                                                                                                         Contact: sapiens@watson.wustl.edu
                                                                                                                                                                              Web site: http://genome.wustl.edu/gsc
                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center Center code: WUGSC
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/db_xref="taxon:9606"
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanaee, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the left is RP11-372J12, the clone sequenced to the right is RP11-588I4. base position 68584 of RP11-259N19. 2000 bp overlap; Actual end is at

FEATURES Polymorphisms have been identifed between AC007387 and AC019069 Location/Qualifiers

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1455: .1675
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7433: .7625
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1873. .5205
   /rpt_family="Alu"
7631. .7650
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1626. .7931
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clone_lib="RPCI-11"
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Homo sapiens Chromosome 16 BAC clone CIT9875K-A-954B10, complete
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Submitted (24-APR-2002) DOE Joint Genome Institute, 2800 Mitchell Submitted, Walnut Creek, CA 94598, USA
Draft Sequence Produced by DOE Joint Genome Institute
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AC119049.1 GI:20279391
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 118521)
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SHGC-103986 G58149.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
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Matches 38; Conservative 0; Mismatches 0;
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4 (bases 1 to 118521)

RS Adams,M.D. and Loftus,B.J.

Direct Submission

AL Submitted (25-JUL-1998) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

On Jul 25, 1998 this sequence version replaced gi:3212841.

Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA e-mail address: humgen@tigr.org. The orientation of the sequence is from sp6 end to T7 end. Genes were identified by a combination of five methods including: XGRAII (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, Mashington), Genscan (Chris B
1048 TAGATTTAAGTAAAAAAAAAAAAAAAAAAAAAAAA 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/cub/hgi/hgi.html). Genes without pepetide homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
3 (bases 1 to 118521)
Adams,M.D. and Loftus,B.J.
Direct Submission
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Adams, M.D., Loftus, B.J.,
Mason, T.M., Brandon, R., 1
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Mason,T.M., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C.
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-954B10
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/db_xref="dbSTS:G02131"
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/note="7617, STS1-cSRL-30a3-uA/cSRL-30a3-uZ,
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
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db_xref="dbSTS:G28812"
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic ı nucleic search, using sw model

Run 8 August 22, 2004, 03:29:28; Search time 514 Seconds (without alignments) 9851.852 Million cell updates/sec

Title: Perfect score: US-10-001-885-31 1192

Sequence: 1 aaaccgcctggagccgccgg.....gaagaggacacacggaaccc 1192

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Word size : 0 Searched:

3373863 seqs, 2124099041 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

6747726

Post-processing: Listing first 45 summaries

N_Geneseq_29Jan04:* geneseqn1980s:*
geneseqn1990s:*
geneseqn2000s:*

geneseqn2003as:*
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SUMMARIES

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ALIGNMENTS

ABN87820 standard; cDNA; 1192 8

ABN87820;

12-AUG-2002

(first entry)

Human ovary specific nucleic acid SEQ ID NO:31.

ovary specific gene; OSG chromosome 10; gene; ss. Human; ovary specific nucleic acid; OSNA; ovary specific protein; OSP; ovary specific gene; OSG; ovarian cancer; immune response; metastasis;

Homo sapiens.

WO200240535-A2

23-MAY-2002.

20-NOV-2001; 2001WO-US045011.

20-NOV-2000; 2000US-0252061P. 27-NOV-2000; 2000US-0253257P.

(DIAD-) DIADEXUS INC.

Salceda S, Macina RA, Recipon Ë Cafferkey ্ষ Sun ĸ Liu Ç

WPI; 2002-471617/50.

New ovary specific genes and proteins, useful as a vaccine for treating patients with ovarian cancer, or for diagnosing and monitoring the presence and metastases of ovarian cancer in a patient.

Claim 1; Page 173-174; 260pp; English.

ABN87790 to ABN87882 represent human ovary specific nucleic acid (OSNA) sequences, and ABB79297 to AB879370 represent ovary specific protein (OSP) sequences from the present invention. OSNA and OSP sequences have cytostatic activity, and can be used in vaccine production and gene therapy. An antibody that specifically binds to an OSP can be used for treating a patient with ovarian cancer, particularly for inducing an immune response against the ovarian cancer cell expressing the CSNA or OSP. The OSNAs and OSPs can also be used for diagnosing and monitoring the presence and metastases of ovarian cancer in a patient

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                                                                      TCAGAGCAAGAAAGCGATGCCCTTCCCAATTCTCTCAATCCTTTTATGCCGAGAAGATCT
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ABL90T ID ABL90 ID ABL90 ID ABL90 ID ABL90 XX ABL90 ID ABL9 XX ABL90 ID ABL90 XX ABL90 ID ABL90 XX ABL90 ID A 밁 Ś S δ 밁 밁 Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorde neurological disease; infection; human; secreted protein; gene; ss. Novel 1405 isolated polypeptides, useful for diagnosis, treatment prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferati disorders. Birse CE, Rosen CA; 18-MAY-2001; 2001WO-US016450 29-NOV-2001. Homo sapiens. Human polynucleotide SEQ ID 24-MAY-2002 ABL90057 (HUMA-) HUMAN GENOME SCI INC. 1021 1141 1081 1081 1021 196 AAAAAGCTGTGGGGGTTACCCGGGGGCCAAAGGGGGGGCCCCGGGGGGGAATGTGGTTCTCC TIGTTTTAATGGTATATTTTTATTGGCTACTTTATTGTTTAGGACAAGTGGTAGTGGCAT 1020 standard; cDNA; 1108 (first entry) ö 619. proliferative 1192 1192 disorder; 1140 1140

Claim 4; SEQ ID NO 619; 2081pp + Sequence Listing; English.

The invention relates to novel genes (ABL8944-ABL90853) and proteins CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating CC (ABB89040-ABB90444) useful for preventing, therapy. The genes are conditions e.g. by protein or gene therapy. The genes are conditions e.g. by protein or gene disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and covarian cancer and other cancers of the adrenal gland, bone, bone marrow, the contract of the protein of: (a) cancer, e.g. breast and covarian cancer and other cancers of the adrenal gland, bone, bone marrow, correct of the contract disease, contract of the contract diseases e.g. cerebral anoxia and epilepsy; and (f) confections. Mote: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly contract of the printed specification, but was obtained in electronic format directly contract of the printed specification, but was obtained precised to the contract directly contract of the printed specification, but was obtained in electronic format directly contract of the printed specification, but was obtained precised to the contract directly contract of the contract of the printed specification, but was obtained precised to the contract directly contract of the contract of the

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Matches 1053; Conserv Sequence 802 899 682 809 622 548 562 488 502 428 368 382 308 322 248 188 128 742 982 848 788 728 8 806 922 82 22 œ 1108 GGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGAGCCGGTGACCTCCATCCTGCT ACCCACAGGGCCTGGGAGGATGGTGGGGATCTTGGGCGAATGGGGGAATCGTGCAGGACGA CTTCCCAATTCTCTCAATCCTTTTATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTC AAGGTATGATCAGAGAGGGGACCACAGGTGTGTGTTTCCCCTTTGTGTTAAGCGTGAGGC GGACTTGCTGGGCCTTGGTGTGAGAGCAGCATATTTGGAGGGGATCTGGTGGTGCCTTG GGACTTGCTGGGCCTTGGTGTGAGAGCAGGCATATTTGGAGGGGATCTGGTGGTGCTTG egrereceacereacreacecereacereacereacecreacecerearacecerrecerrereacac GSTSTCCCACCTGAGTCAGCGSTGACCTCTGAGGGCTGATAGGGGTTGGTTTGTTGAGAG TGCCAGGCTGGGTGCTCAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGTGAACAT TGCCAGGCTGGGTGCTCAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGTGAACAT CGACCCCGGAGTGAGGACCACTACCCAGCCAGCCAAGAGGTAGCATTCCTCGACAGAGCTT CGATGCCTGTGGAAGACATGCCGACGTCTCCTCTGCCTAGGGAGCAGGACTTGGGCTTAG Conservative BP; 234 A; 75.8%; 99.7%; 274 ٥, Score 903; DB 6 Pred. No. 0; 0; Mismatches ç; 324 و. 271 T; 0 ٠. ص **ω** Length 1108; U; 5 Other; Indels 0, Gaps 67 381 321 247 261 187 141 561 501 427 441 367 307 1041 801 667 681 607 621 547 487 981 921 847 861 727 741 967

> 밁 ঠ 1028 1042 AATAAATAGATTTAAGTAAAAAAAAAAAAAAAAAAA AATAAATAGATTTAAGTAAAAAAAAAAAAAAAA 1077

AAV59558 standard; DNA;

06-JAN-1999 (first

secreted protein gene 48 clone HFCAI74.

RESULT 3

AAVS124

AAVS2458

AAVS2458

AC AAVS2

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WO9839448-A2

07-MAR-1997; 07-MAR-1997; 97US-0038621P 98WO-US004493

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12-MAY-1999;
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AAV59558

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; schaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens.

11-SEP-1998

07-MAR-1997; 07-MAR-1997;

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23-MAY-1997
23-MAY
                     WPI; 1998-506364/43.
P-PSDB; AAW74778.
                                                                 Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC; Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PB, (Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 66.4%; Score 792; DB 2; I Best Local Similarity 99.8%; Pred. No. 5.1e-302; Matches 1032; Conservative 0; Mismatches 0;
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                                                    CAGGTGTGTGTTTCCCCCTTTGTGTTAAGCGTGAGGCAGAGGGGAGACGTTAGT-CCAGCAT
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                                    CAGGTGTGTGTTTCCCCCTTTGTGTTAAGCGTGAGGCAGAGGGAGACGTTAGTCCCAGCAT
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New isolated human

genes and the secreted polypeptide(s) they

RESULT 4
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XX ABS77
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XX 8 8 8 8 8 밁 8 8 8 유양 07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 07-MAR-1997 11-APR-1997 Human; ss; gene; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral ischaemia; anglogenesis; sunburn; nervous system disorders; Alzheimer's disease; infection; coular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive; preservative; nutritional. Human ABS73545 08-SEP-1998; 16-JUL-2002. US6420526-B1 15-JAN-2003 ABS73545; 1004 sapiens 961 901 884 781 824 721 764 CDNA standard; CTTTTTAGCACTGTTTTTGTTTTAATGGTATATTTTTATTGGCTACTTTATTGTTTAGG GACGTCTCCTCTGCCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGA GACGTCTCCTCTGCCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGA TTATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCC TTATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCC CATTAAGTGGCACAAAATCAGAAGCAAGAAAGCGATGCCCTTCCCAATTCTCTCAATCCTT CATTAAGTGGCACAAAATCAGAGCAAGAAAGCGATGCCCTTCCCAATTCTCTCAATCCTT CTTTTTTAGCACTGTTTTGTTTTAATGGTATATTTTTATTGGCTACTTTATTGTTTAGG #1 for (first 98US-00149476 novel secreted cDNA; 3-0040334P.
3-0040336P.
3-00410326P.
3-0043311P.
3-0043312P.
3-0043313P.
3-0043314P.
3-0043315P.
3-0043315P.
3-0043569P.
3-0043576P.
3-0043578P.
3-0043570P. 3-0040162P. S-0040163P. S-0040333P. -0040161P -0038621P entry) 1049 BP protein gene 48. 1063 1003 960 900 943 840 883 823 780

PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043674P.
PR 11-APR-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0056632P.
PR 23-MAY-1997; 97US-0056632P.
PR 23-MAY-1997; 97US-0056632P.
PR 23-MAG-1997; 97US-0056632P.
PR 23-MUG-1997; 97US-0056632P.
PR 22-MUG-1997; 97US-005663P.
PR 22-MUG-1997; 97US-0056684P.
PR 22-MUG-1997; 97US-005688P.
PR 22-MUG-1997; 97US-005689P.
PR 22-MUG-1997;

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22-AUG-1997;
05-SEP-1997;
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12-SEP-1997;
02-OCT-1997;
06-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1049 BP; 223 A; 258 C; 303 G; 265 T; 0 U; 0 Other;
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                                                                         CCAGCCAACCAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCC
                                                                                                                                           GCGGATCTTGGCCAATGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACCACTAC
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R, Endress GA, Yu G, Ni J, Feng P, Young PE,
Duan R, Hu J, Florence KA, Olsen HS, Ebner I
Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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Pred. No. 5.1e-302;
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Human; secreted protein; hyperproliferative disorder; leukaemia; breast cancer; wound; reproductive disorder; blood-related disorder; haemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia; wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis; graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma; viral infection; bacterial infection; fungal infection; AIDS; sepsis; renal disorder; kidney failure; cardiovascular disorder; cytostatic; and a sorder; kidney failure; cardiovascular disorder; cytostatic;
                                                                                                                                                                                   cDNA sequence #48 containing coding region of a human secreted protein.
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CATTAAGTGGCACAAAATCAGAGCAAGAAAGCGATGCCCTTCCCCAATTCTCTCAATCCTT
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111-APR-1997
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23-MAY-1997
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Ruben SM,
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08-JUL-1997;
16-JUL-1997;
18-AUG-1997;
                                          (ZENG/)
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CARTER K C.
BEDNARIK D P.
ENDRESS G A.
YU G.
NI J.
FERG P F.
GREENE J M.
FERRIE A M.
DUAN D R.
HU J D.
FLORENCE K A.
OLSEN H S.
FISCHER C L.
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BREWER L A.
MOORE P A.
SHI Y.
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LI Y.
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97US-0056631P.
97US-0056632P.
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           Soppet DR,
             Carter
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           Bednarik DP;
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The present invention relates to the isolation of novel human secreted CC proteins and the polynucleotide sequences encoding them. The invention CC also discloses vectors, host cells, antibodies, and recombinant methods CC for producing human secreted proteins. The polypeptide and polynucleotide CC sequences for the secreted proteins. The polypeptide and polynucleotide CC ameliorating or diagnosing medical conditions such as hyperpoliferative CC disorders (e.g. leukaemia or breast cancers), wounds, reproductive CC disorders, blood-related disorders (e.g. haemophilia or CC thymic hypoplasia), autoimmune disorders (e.g. wiskott-Aldrich syndrome or thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease, CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma), CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. angina CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina pectoris, cerebral ischaemia or congenital heart defects), respiratory CC disorders, neurological disorders (e.g. Alzheimer's disease or CC parkinson's disease), and inflammations (e.g. Crohn's disease). The CC polynucleotide or polypeptide may also be used as vaccine adjuvants. CC MOB2641-ACD82950'encode human secreted proteins or their fragments. CC specification, but was obtained in electronic format directly from the crossory as size at each seafular austra CC/Mainanniberry. Amil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1049 BP; 223 A; 258 C; 303 G; 265 T; 0 U; 0 Other;
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TGTTCGTGGCCTCCTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTG
                                                                         CAACCATGCTGTGGAGCCGGTGACCTCCATCCTGCTCCTCCTGCTCATGATGCTTGG
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1 J, Florence KA, Olsen HS, Fischer CL, Ebner
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, F
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Pred. No. 5.1e-302;
0; Mismatches 0;
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                                                               GACGTCTCCTCTGCCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAATTCCAGA
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Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infective arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoac
                                                                                                                    WO200270539-A2
                                                                                                                                                                       antiarthritic;
                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 94.
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05-MAR-2001; 2001US-00799451 05-MAR-2002; 2002WO-US005095.

L2-SEP-2002.

Tang ጀ , Zhou P, Yang Y, T, Wang J Ma Goodrich .RW, Asundi V, Zh Ma Y, Yamazaki V, Chen R, Wang D, Drmanac RT; Zhang J, Z R, Wang Z, Zhao QA, , Ghosh M; Ren 'EJ

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TGAGAGGGACTTGCTGGGCCTT 577

New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p coagulation disorders. or platelet

Claim 1; SEQ ID NO 94; 1012pp + Sequence Listing; English

muleotide sequence selected from any of 948 sequences (ABZ11119C ABZ12066) or their mature protein coding portion, active domain coding
protein or complementary sequences. The polynucleotides are useful for
identifying expressed genes or for physical mapping of human genome. The
c encoded polypeptides (ABP68902-ABP6984) are useful as molecular weight
c markers, as a food supplement, for generating antibodies, in medical
imaging, screening and diagnostic assays and for treating cellproliferative disorders (cancer), neurodegenerative diseases (Parkinson's
c proliferative disorders (cancer), neurodegenerative diseases,
c r Alzheimer's disease), autoimmune diseases (multiple sclerosis,
c r Alzheimer's disease), autoimmune diseases (multiple sclerosis,
c platelet or coagulation disorders, myeloid or lymphoid disorders, liver
c platelet or coagulation disorders, wound, burns, incision, ulcers, liver
c platelet or coagulation disorders, wound, burns, incision, parastic),
c platelet or coagulation disorders, myeloid or long fibrosis, infections (bacterial, viral, fungal, parastic),
c platelet or coagulation disorders, myeloid or long fibrosis, infections (bacterial, viral, fungal, parastic),
c printed specification, but was obtained in electronic format
c directly from WIPO at ftp.wipo.int/pub/published_pct_sequences relates to an isolated polynucleotide (I) comprising Ø

Sequence 562 BP; 95 A; 176 C; 174 G; 117 T; 0 U; 0 Other;

Length 562;

밁 8 밁 Ş ß 멂 Ś δ 밁 Ś Ś 중 유 Š 닭 밁 S Query Match Best Local S Matches 562 481 496 421 436 361 376 301 316 241 181 196 136 256 121 562; 61 76 16 Similarity TCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAATGGGGAAATCGTGCA 195 GTGGGTCACCTCTGTGAACATCACTGACTGCAAGCCCTCCAATTTCTGGTGCAGCCCA CCTGCTCCTCCTGCTCATGATGCTTGGTGTTCGTGGCCTCCTCCTGGTTGGCCTTGT GAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGAGCCGGTGACCTCCAT GAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGAGCCGGTGACCTCCAT GGACGACGACCCCGAGTGAGGACCACTACCCAGCCACCAAGAGGTAGCATTCCTCGACA GCCGGGAGTGGACGCCGGAGGCCCGGAGTCGCGCCTGCAGACACAGCATCTACTCAGC GCCGGGAGTGGACGCCGGAGGCCCGGAGTCGCGCCTGCAGACACAGCATCTACTCAGC CTACCTGGTGTCCCACCTGAGTCAGCGGTGACCTCTGAGGGCTGATAGGGGTTGGT CTACCTGGTGTCCCCACCTGAGTCAGCGGTGACCTCTGAGGGGCTGATAGGGGTTGGT GCAGGTGCCAGGCTGGTGCTGAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGT GGCAGGTGCCAGGCTGGGTGCTCAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGT GGACGACCACCCCGAGTGAGGACCACTACCCAGCCAAGAGGGTAGCATTCCTCGACA Conservative 47.1%; 5 100.0%; Pr Score 562; DB 6; Le ; Pred. No. 1.8e-211; Mismatches Indels 0 Gaps 495 255 120 240 180 540 480 420 360 300 60

300

240 286 180 226 120 166 60

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δ 뮍 Ś 跊 8 片 Ś 片 맑 Matches Query Match Best Local : The present sequence encodes a breast tumour-associated protein. It was shown to have at least two-fold overexpression in breast tumour tissue. The invention relates to an isolated polypeptide comprising at least an immunogenic portion of a breast tumor-specific protein, or its variant that retains the ability to react with antigen-specific antisers. The breast tumour polymucleotides, polypeptides and antibodies are useful for inhibiting development of breast cancer. The polymucleotides may be used to design primers and probes for detecting and monitoring breast cancer New polypeptides encoded by polynucleotide sequences over-expressed breast tumor tissue are useful to detect, monitor and treat breast 11-OCT-2000; 2000WO-US028255 WO200127276-A2 Human; Human breast tumour protein cDNA 15964. 18-JUN-2001 AAF82505 Claim 13; Page 50; 52pp; English. WPI; (CORI-) CORIXA CORP. 12-OCT-1999; 19-APR-2001. AAF82505; 2001-273773/28 sapiens 181 121 541 227 167 107 369; 61 47 breast cancer; tumour; cytostatic; gene therapy; ss Similarity 550 AAGCCTCCCTCAATTTCTGGTGCAGCCCATCAGGGACCCACAGCGCCCTGGGAAGGATGGTG standard; cDNA; CGGATCTTGGCCAATGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACCACTACC CCAGGGGGTCCTGGCCCCCCCCCAGCAGCAGCAGGCAGGTGCCAGGCTGGGTGCTCAGTCC CAGCCACCAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCCC CAGCCACCAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCCATGGTGCTCCC CGGATCTTGGCCAATGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACCACTACC AAGCCTCCCTCAATTTCTGGTGCAGCCCATCAGGGACCCACAGCGCCCTGGGAGGATGGTG SL, Conservative BP; 102 (first 99US-00417031. Dillon 31.0%; bu 100.0%; Pr entry) A; 163 C; 164 G; 118 T; 0 U; 'n, 550 ž Score 369; Pred. No. BP Ç Mismatches 562 1.6e-135; DB 4; Length 550 w Indels Other; 0; Gaps ä

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RESULT 8
ABSY92251
ID ABSY9
XX ABX9
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                                                                                                                                                                                 The invention relates to a new isolated nucleic acid termed ovarian consecution specific nucleic acid (OSNA) comprising: (a) a nucleic acid molecule that concides any of 53 fully defined protein sequences appearing as ABU61018-CR ABU61070 (termed ovarian specific proteins, OSP); (b) any of 76 fully defined nucleotide sequences appearing as ABU92187-ABU92262; or (c) a sequence having at least 60% sequence identity to the nucleic acid molecule of (a) or (b). Also included are a method for determining the comprising an OSNA, a host cell comprising the vector, an isolated OSP polypeptide, an anti-OSP antibody or fragment, a method for determining the presence of an ovary specific protein in a sample and vaccine comprising an OSP or OSNA. The methods and compositions of the present congrising an OSP or OSNA. The methods and compositions of the present invention are useful for identifying, diagnosting, monitoring, staging, imaging and treating ovarian cancer and non-cancerous disease in ovary consisted. The present sequence is an OSNA of the invention
Query Match
Best Local S
Matches 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 185-186; 224pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated OSNA nucleic acid and encoded polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous diseases in ovarian tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salceda S,
Sun Y, Liu
                                                                                                                               Sequence 365 BP; 60
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P-PSDB; ABU61063.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ovarian specific nucleic acid DEX0310_65.
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15-FEB-2001; 2001US-0268834P.
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                                      Similarity
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C;
   27.3%; Score 326; DB 7; Lilarity 100.0%; Pred. No. 1.4e-118; Conservative 0; Mismatches 0;
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                                                                                                                                   A; 117 C; 108 G; 80 T; 0 U; 0 Other;
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                                                                   Length 365;
          Indels
       <u>,</u>
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200 GACGACCCCCGAGTGAGGACCACCACCAGCCAGCCAAGAGGTAGCATTCCTCGACAGAGGC

259

The present invention relates to a microarray comprising a matrix of at least one cDNA probe from a set of probes immobilised to a solid surface in a predetermined order, where a row of pixels corresponds to replicates of one distinct probe from the set. The probes are complementary to mucleic acid sequences that are expressed differentially in aggressive as compared to non-aggressive types of clear cell renal carcinoma (CC-RCC) and that hybridise to the probes under high stringency conditions. The microarray is useful for the prognosis of patients with CC-RCC, wherein aggressive and non-aggressive CC-RCC tumour types are characterised by differential expression profiles of genes that hybridise with one or more probes immobilised on the microarray. The arrays are useful for gene expression profiling of tumour and normal tissues. The present sequence represents a human cDNA sequence differentially expressed in aggressive

Claim 1; SEQ ID NO 459; 179pp; English.

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RESULT 9
ABX74673/c
ID ABX74673;
XX AC ABX74673;
XX 21-MAR-200
XX 21-MAR-200
XX Human; mic
KW differenti
KW non-aggres
KW gene expre
OS Homo sapie
XX 10-OCT-200
XX 10-OCT-200
XX 29-MAR-200
XX 29-MAR-200
XX 29-MAR-200
XX 29-MAR-200
XX Wew microa
PT Haab B, R
XX Wew microa
PT Haab B, R
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PT immobilize
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CC Itast one
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CC expression
                                                                                                                                                                                                                                                                                                                             New microarray, comprising a matrix of cDNA probe from a set of probes immobilized to a solid surface in predetermined order, useful in the prognosis of patients with clear cell renal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; microarray; solid surface; immobilised probe; CC-RCC; differential expression profile; aggressive CC-RCC tumour type; non-aggressive CC-RCC tumour type; clear cell renal carcinoma; gene expression profiling; tumour tissue; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-040679/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA sequence #128 differentially expressed in CC-RCC types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (VAND-) VAN ANDEL INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; cDNA; 517 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takashi M;
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RESULT 10
ABX9250
ID ABX92250
XX ABX92
XX ABX92
AC ABX92
XX Human
CC ABMCC
ID ABX92
AC ABX92 Ś Ś 음 성 뭥 S 망 밁 SXS Query Match Best Local Simi Matches 285; Sequence gynaecological. 08-MAY-2003 (first entry) ABX92250; ABX92250 standard; vs. non-aggressive type CC-RCC phenotypes The invention relates to a new isolated nucleic acid termed ovarian specific nucleic acid (OSNA) comprising: (a) a nucleic acid molecule that encodes any of 53 fully defined protein sequences appearing as ABU61018-ABU61070 (termed ovarian specific proteins, OSP); (b) any of 76 fully defined nucleotide sequences appearing as ABX92187-ABX92262; or (c) a New isolated OSNA nucleic acid and encoded polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous diseases in ovarian tissues. WO200292785-A2. Human; gene; ss; ovarian specific nucleic acid; OSNA; ovarian cancer; non-cancerous ovarian disease; gene therapy; vaccine; cytostatic; 13-FEB-2001; 2001US-0268290P. 15-FEB-2001; 2001US-0268834P. 13-FEB-2002; 2002WO-US022271. 21-NOV-2002 Claim (DIAD-) DIADEXUS 503 2003-120677/11. 207 743 267 683 327 623 387 563 447 ovarian 1; Page 185; 224pp; English Similarity S, Macina Liu C; ABU61062. GACTTGCTGGGCCTTGGTGTGAGAGCAGGCATATTTGGAGGGGATCTGGTGGTGCCTTGA 517 GACTTGCTGGGCCTTGGTGTGAGAGGCAGGCATATTTGGAGGGGATCTGGTGCCTTGA TTTTAGGTGGTATGGGGCCTGCATTAAGTGGCACAAAATCAGAGCA 788 AGGTATGATCAGAGAGGGGGACCACAGGTGTGTGTGTTTTCCCCTTTGTGTTTAAGCGTGAGGCA TTTTAGGTGGTATGGGGCCTGCATTAAGTGGCACAAAATCAGAGCA 162 AGGTATGATCAGAGAGGGGACCACAGGTGTGTGTTTCCCCCTTTGTGTTAAGCGTGAGGCA 19.7%; ilarity 99.7%; Conservative BP; 166 A; 154 C; 90 G; 107 T; 0 U; 0 Other; specific nucleic acid DEX0310_64. INC RA, CDNA; Hu 612 'n 0; Score 235; DB 7; Pred. No. 8.8e-83; 쁑 Recipon H, Mismatches Karra Length 517; <u>,</u>× Indels Cafferkey 0 ø Gaps 682 328 388 208 268

> ₽ / 8888888888888888 8 밁 5 Ś 밁 S 밁 Matches Query Match Best Local sequence having at least 60% sequence identity to the nucleic acid molecule of (a) or (b). Also included are a method for determining the presence of an ovary specific nucleic acid (OSNA) in a sample, a vector comprising an OSNA, a host cell comprising the vector, an isolated OSP polypeptide, an anti-OSP antibody or fragment, a method for determining the presence of an ovary specific protein in a sample and a vaccine comprising an OSP or OSNA. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous disease in ovary tissue. The present sequence is an OSNA of the invention Sequence 612 BP; 156 A; 120 C; 171 G; 165 T; 0 U; 0 Other; 1008 441 948 321 888 261 GCCGAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACG 828 GCCGACAACAACATGTTCCGATGCCTGTGGAAGACATGCCGATGCCTGTGGAAGACATGCCGACG 195; Similarity TTTAGCACTGTTTTTGTTTTTAATGGTATATTTTTATTGGCTACTTTATTGTTTAGGACAA 1007 rcrccrcrccchagegaecaceacrrggecrragegcaegregaaaaaarrccagacrr TCTCCTCTGCCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTT GTGGTAGTGGCATTC GIGGIAGIGGCATIC 16.4%; Score 195; llarity 100.0%; Pred. No. Conservative 0; Mismatch 455 1022 Mismatches 4.7e-67; DB 7; Length 612; Indels 0; Gaps 947 440 380 320 887

RESULT 11 AAS64820 AAS64820 standard; cDNA; 1165 묤

AAS64820;

13-FEB-2002 (first entry)

DNA encoding novel human diagnostic protein #624

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

WO200175067-A2

11-0CT-2001.

30-MAR-2001; 2001WO-US008631.

31-MAR-2000; 23-AUG-2000; 2000US-00540217. 2000US-00649167.

HYSEQ INC.

RT, Liu ņ Tang Ţ,

P-PSDB; 2001-639362/73.)B; ABG00633.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ij g 624; 103pp; English

invention relates ö isolated polynucleotide Ĥ and polypeptide (II)

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RESULT 12
AAS64819/c
ID AAS648
XX AAS648
XX DNA en
XX DNA en
XX Human;
KW Human;
KW Hood s
XX Homo s
XX Ho
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Best Local :
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                                                                         WPI; 2001-639362/73.
P-PSDB; ABG00632.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #623
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New isolated polynucleotide and encoded polypeptides, useful in

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. 30-MAR-2001; 2001WO-US008631.

(HYSE-) HYSEQ INC

Homo sapiens.

11-0CT-2001 WO200175067-A2 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;

88

DNA encoding novel human diagnostic protein #625

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ARSGULT 13
ARS64821
ID ARS64
XX ARS64
XX ARS64
XX IN-FE
XX DNA e
XX Human
KW Homo
XX Homo
XX Homo
XX HOMO
PN WO200
XX IN-OC
XX 30-M3
XX 31-M3
PF 31-M4
PR 31-M4
PR 33-M1
XX HYSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 159; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS64821 standard; cDNA; 587 BP
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WPI; 2001-639362/73. P-PSDB; ABG00634.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Claim 1; SEQ ID NO 625; 103pp; English

cc genes. (I) is useful in gene therapy techniques to restore normal cc genes. (I) is useful in gene therapy techniques to restore normal cc useful for generating antibodies against it, detecting or quantitating a cc useful for generating antibodies against it, detecting or quantitating a cc golypeptide in tissue, as molecular weight markers and as a food cc golypeptide in tissue, as molecular weight markers and as a food cc sites expressing (II). (I) and (II) are useful in medical imaging co f sites expressing (II). (I) and (II) are useful for treating disorders cinvolving abservant protein expression or biological activity. The cc polypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cc diagnostics, forensics, gene mapping, identification of mutations cc and to produce other types of data and products dependent on DNA and camino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this cc coding sequences of the invention. Note: The sequence data for this cc patent did not appear in the printed specification, but was obtained in ce lectronic format directly from WIPO at The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed ftp.wipo.int/pub/published_pct_sequences

Sequence 587 BP; 147 A; 106 C; 166 G; 168 T; 0 U; 0 Other;

ঠ 멂 Ś 밁 Ś 밁 Query Match Best Local S Matches 157 1027 967 414 907 157; Similarity TATTGTGACCTTTTCAATAAATAGATTTAAGTAAAAA ТАТТСТСАССТТТТСААТАААТАСАТТТААСТАААА 1063 TAATGGTATATTTATTGGCTACTTTATTGTTTAGGACAAGTGGTAGTGGCATTCTATT TAATGGTATATTTTATTGGCTACTTTATTGTTTAGGACAAGTGGTAGTGGCATTCTATT AGGACTTGGGCTTAGGGCAGGTGGAAAAATTCCAGACTTTTTAGCACTGTTTTTGTTT AGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTTTTTTAGCACTGTTTTTGTTT Conservative 13.2%; Score 157; DB; Pred. No. 4.3 0, 4.3e-52; DB ű, 0 570 Length 587; Indels ٥, Gaps 1026 966 533 473

RESULT 14
ABN87819
ID ABN87
XX ABN87
AC ABN87
XX 12-AL
XX Humar
XX Humar
XX Grae
COS Homo
XX Grae
XX G

ABN87819 standard; cDNA; 643 뫄

12-AUG-2002 (first entry)

Human ovary specific nucleic acid SEQ ID NO:30.

gene; ovary Human; ovary ; ovary specific nucleic acid; OSNA; ovary specific protein; OSP; specific gene; OSG; ovarian cancer; immune response; metastasis;

Homo sapiens

WC200240535-A2

23-MAY-2002

20-NOV-2001; 2001WO-US045011.

20-NOV-2000; 2000US-0252061P. 27-NOV-2000; 2000US-0253257P. (DIAD-) DIADEXUS INC.

Salceda S, Macina RA, Recipon H, Cafferkey R, Sun ĸ Ç

New ovary specific genes and proteins, useful as a vaccine for patients with ovarian cancer, or for diagnosing and monitoring presence and metastases of ovarian cancer in a patient. treating

Claim 1; Page 173; 260pp; English.

ABN87790 to ABN87882 represent human ovary specific nucleic acid (OSNA) sequences, and ABB79297 to ABB79370 represent ovary specific protein (OSP) sequences from the present invention. OSNA and OSP sequences have cytostatic activity, and can be used in vaccine production and gene therapy. An antibody that specifically binds to an OSP can be used for treating a patient with ovarian cancer, particularly for inducing an immune response against the ovarian cancer cell expressing the OSNA or OSP. The OSNAs and OSPs can also be used for diagnosing and monitoring the presence and metastases of ovarian cancer in a patient

Sequence 643 BP; 170 A; 139 C; 172 G; 162 T; 0 U; 0 Other;

S 밁 Ś 밁 Ś 닭 Query Match Best Local Matches 125; 948 335 888 275 828 395 Similarity GCCGAGAAGATCTCAGCTGGATGCCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACG TCTCCTCTGCCTAGGGAGCAGGACTTGGGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTT TTTAG TTTAG TCTCCTCTGCCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTT Conservative 399 952 10.5%; <u>,</u> Score 125; Pred. No. Mismatches DB 6; Le. . 1.7e-39; . 7 0; Length 643; Indels 0, Gaps 887 947 334 0

AAI16223 standard; DNA; 473

AAI16223;

12-OCT-2001 (first entry)

#6156 for gene expression analysis in human cervical cell sample

Probe; human; microarray; gene expression; cervical epithelial ${\tt celi}_i$; cervical cancer; ${\tt ss}$.

sapiens

WO200157278-A2

09-AUG-2001.

04-FEB-2000; 26-MAY-2000; 30-JUN-2000; 03-AUG-2000; 21-SEP-2000; 27-SEP-2000; 04-OCT-2000; ; 2000US-0180312P. 2000US-0207456P. 2000US-00608409. 2000US-00632366. ; 2000US-0032365. ; 2000US-0236359P. 2000US-0236359P. 2000US-0236359P.

30-JAN-2001; 2001WO-US000670.

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Search completed: August 22, 2004, 05:00:50 Job time: 520 secs
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                                                                                                                                                                 Query Match 3.2%; Score 38; DB 4; Length 473; Best Local Similarity 100.0%; Pred. No. 3e-05; Matches 38; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at itp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                             Sequence 473 BP; 153 A; 80 C; 101 G; 139 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 6156; 487pp; English.
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                                                                                                          1048 TAGATTTAAGTAAAAAAAAAAAAAAAAAAAAAAA 1085
                                                                                259 TAGATTTAAGTAAAAAAAAAAAAAAAAAAAAAAAA 296
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Title:
Perfect score:
Sequence:
                                                                                                           Database :
                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                  Scoring table:
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                                                                                                                                                                                                                                                                                               OM nucleic -
                                                                                                                         Post-processing: Listing first 45
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Gapop 60.0 , Gapext 60.0
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1192
1 aaaccgcctggagccgccgg.....gaagaggacacacggaaccc 1192
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11881.081 Million cell updates/sec
                                                                                                                                                                                            27513289 seqs, 14931090276 residues
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em_estba:*
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BF569253 602184629
BG331398 602433369
BM459665 AGENCOURT
CA942743 ir66f05.x
BE904302 601494571
AIZ88133 g190e03.x
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AW955776 EST364846
BG055477 nad54h01.
BX095713 BX095713
BU7933254 UI-E-C11
AA682907 ae88g03.8
AA398343 zt61d05.8
AA397331 0e660C01.8
BM77494 UI-E-EJ0-BM774136 UI-E-EJ0-BM774136 UI-E-EJ0-BM774136 UI-E-EJ0-BM713798 III3-H7061 S1
AA197950 g153a10.x
AIG94330 w445e08.x
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AIG94330 w455067.x
AIG9630 wx35c07.x
AIG9630

9910113113

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_estfun:*
em_gss_inv:
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SUMMARIES

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ć	502	510	586	630	1 1 1 1 1 1 1	Score		
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	JOURNAL MEDLINE PUBMED COMMENT	REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BM675290/c LOCUS DEFINITION
COORDINATED LABORATORY FOR COMPUTATIONAL GENOMICS University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu Tissue Procurement: Dr. Gregy Hageman	Alsocovery Genome Res. 6 (9), 791-806 (1996) 97044477 8889548 Contact: Soares, MB	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 708) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene	UI-E-EJO-ahr-n-23-0-UI 3', mRNA sequence. BM675290 BM675290.1 GI:18985188 EST. Homo sapiens (human) Homo sapiens	BM675290 708 bp mRNA linear EST 27-FEB-2002 UI-E-EJO-ahr-n-23-0-UI.sl UI-E-EJO Homo sapiens cDNA clone

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FEATURES
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Best Local S
Matches 680
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The following repetitive elements were found in this cDNA sequence: 1-42, >AT_rich#Low_complexity (matched compliment) Seq.primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                           GGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGAGCCGGTGACCTCCATCCTGCTC
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TTTTAGGTGGTATGGGGCCTGCATTAAGTGGCACAAAATCAGAGCAAGAAAGCGATGCCC
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Conservative
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/clone="UI-B_EUG-ahr-n-23-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
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/mol_type="mRNA"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 688)

E NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Unpublished (1999)

Unpublished (1999)

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11554 row: i column: 19
High quality sequence stop: 688.
1 688
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688 bp mRNA linear EST 29-AUG
603081177F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5220570
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                           Conservative
                                                                                                                       /clone lib="NTH_MGC_120"
/clone lib="NTH_MGC_120"
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pCMV-SPORTG; Site 1: NotI; Site_2: EcoRV (destroyed); RNA
pCMV-SPORTG; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:5220570"
/lab_host="DH108"
                           49.2%; Score 586; DB 12; 99.7%; Pred. No. 6.6e-109; tive 0; Mismatches 2;
                                                               Length 688;
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5629.f
more information about this cluster, see
http://www.genoscope.cns.fr/
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                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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BQ884216 892 bp mRNA
AGENCOURT 8681949 Lupski_sciatic_nerve
IMAGE:6197459 5', mRNA sequence.
BQ884216 BQ884216.1 GI:22276224
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="fomo sapiens FETAL BRAIN"
/note="Organ; brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECCRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 8.6e-94;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM.3607 row: i column: 12
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1 (Dases 1 to 892)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                     GAGGGCTGATAGGGGTGTGGTTTGTTGAGAGGGGACTTGGTGGGCCTTGGTGTGAGAGCAGG
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                                                                                                                                                                                                                                                                                             TGCTGTGGAGCCGGTGACCTCCATCCTGCTCCTTCCTGCTCATGATGCTTGGTGTTCG
TGTGTTTCCCCTTTGTGTTAAGCGTGAGGCAGAGGGAGACGTTAGTCCAGCATTTCCAAA
                TGTGTTTCCCCTTTGTGTTAAGCGTGAGGCAGAGGGAGACGTTAGTCCAGCATTTCCAAA
                                                                                            CATATTTGGAGGGGATCTGGTGGTGCCTTGAAGGTATGATCAGAGAGGGGGACCACAGGTG
                                                                                                                                                                                                  TGGCCTCCTCCTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTGACCTCT
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                                                                CATATTTGGAGGGGATCTGGTGGTGCCTTGAAGGTATGATCAGAGAGGGGACCACAGGTG
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="Lupki sciatic nerve"
//clone lib="Lupki sciatic nerve"
//note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
Not; Site 2: Sal; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5:-TCGACCCACGCTCCG-3' and
5:-GACTAGTTCTAGATCGCACGCGCCGCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
Technologies."
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/dev_stage="adult, 70 yr"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 3.6e-92;
0; Mismatches 2;
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                                                                                                     Similarity
                                       GGAGCCGCCGGGAGTCGCACGCCGCCGAGGCCCGGAGTCGCGCCCTGCAGACACCAGCATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCT 895
                                                                                   41.2%;
llarity 99.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:9606"
                                                                                   Score 491; DB Pred. No. 7.2e 0; Mismatches
                                                                                   DB 10;
7.2e-90;
hes 1;
                                                                                                                     Length 714;
                                                                                       Indels
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CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1159 row: j column: 07 High quality sequence stop: 712. Location/Qualifiers
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1 (Dases 1 to 714)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:4300518"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="PHIOB (phage-resistant)"
/clone_lib="NIH_MGC_42"
/clone_lib="NIH_MGC_42"
/clone_lib="NIH_MGC_42"
/clone_lib="NIH_MGC_42"
/clone="forgan: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EGORI; cDNA made by oligo-dT prining.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Size-selected >500bp
for average insert size_1.8bb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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AUTHORS
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VERSION
KEYWORDS
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                                                                                                                       source
                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1244 row: j column: 17
High quality sequence stop: 638.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1104)
11 (bases 1 to 1104)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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EST.
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602433369F1 NIH_MGC_18 Homo e
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/clone="IMAGE:4550896"
/tissue_type="large cell carcinoma"
/lab host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_18"
                                                                                                                   .1104
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sapiens
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/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: ECCRI; cDNA made by Oligo-dT priming. Directionally cloned into EccRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript I RT (Life Technologies). Note: this is a NIH_MGC Library."
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Similarity 41.2%; ilarity 99.8%; Conservative Score 491; DB 12; Pred. No. 4.7e-90; 0; Mismatches 1; Length 1104;

밁 S 밁 S 밁 Ś 닭 Ś 밁 5 멁 S 밁 8 밁 Ś 문 Query Match Best Local Sim Matches 541; 541 550 481 490 421 430 361 370 301 310 181 121 190 130 61 70 10 μ GT 551 ម្ន GCAGCAGGCAGGCCAGGCCGGGTGCTGCTCAGTCCCCCCTTCAATGACCTCAACCGGCA AGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAATGGGGAAAT CCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTGACCTCTGAGGGCTGATAGGGGTGG CCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTGACCTCTGAGGGGCTGATAGGGGTGG GCTGGTGAACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGAGCCGGTGAC GCAGCAGGCAGGCTGCGGTGCTCAGTCCCCCTTCAATGACCTCAACCGGCA TCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCCCCAGGGGGTCCTGGCCCCCGCCA GGAGCCGCCGGAGTGGACGCCGCCGAGGCCCGGAGTCGCCCTGCAGACACAGCATCTA GGAGCCGCCGGGAGTGGACGCCGCCGACGCCCGGAGTCGCGCCTGCAGACACACCATCTA crecarecrecrecrecrecrearearecrieererreerecreerecreerree crccarecrecrecrecrecrearearecreererreerecreerecrecreerree TCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCCCCCAGGGGGTCCTGGCCCCCGCCA CGTGCAGGACGACCACCCCGAGTGAGGACCACTACCCAGCCACCAAGAGGTAGCATTCC AGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGGCCAATGGGGAAAT 542 Indels 0 Gaps 189 60 540 549 480 489 429 360 369 300 309 240 249 120 129 420 180 0

RESULT 7 BM459665 LOCUS DEFINITION

linear EST 05-FEB-2002 DNA clone IMAGE:5534295

Euteleostomi;
; Homo.

KEYWORDS SOURCE ORGANISM VERSION ACCESSION AGENCOURT 6417963 NIH MGC_71 Homo sapiens cDNA 5'; mRNA sequence.
BM459665 BM459665.1 GI:18508705

REFERENCE AUTHORS TITLE JOURNAL COMMENT

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 937)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collec Unpublished (1999)
Contact: Robert Strausberg, Ph.D. Gene Collection (MGC)

Email: cgapbs-r@mail.nih.gov

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FEATURES
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Best Local Similarity 99:
Matches 634; Conservative
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12220 row: i column: 16
High quality sequence stop: 585.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                AATTCTCTGAATCCTTTTATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGC 867
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/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. "
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/db_xref="taxon:9606"
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VERSION
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 541)

2 (cemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Marrin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

Milliams, T., Jackson, Y. and Bowers, Y.

Bridocrine Pancreas Consortium

Unpublished (2000)

Other_ESTs: ir66f05.y1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                       421
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                                                                                                                                                                                                                                                                  591 GCATATTTGGAGGGGATCTGGTGGTGGTGCCTTGAAGGTATGATCAGAGAGGGGACCACAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
Seq quality sequence stop: 455.
Location/Qualifiers
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Libbary was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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/clone libe HR85 islet"
/note=Torgan: Pancreas; Vector: pBluescript SK(-); Site_1:
/note=Torgan: Pancreas; Vector: pBluescript SK(-); 
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/mol_type="mRNA"
/db_xref="raxon;9606"
/clone="IMAGE:6607449"
/tissue_type="purified pancreatic islet"
/lab_host="DH103"
/clone_lib="HR85_islet"
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	40.3%; Score 480; DB 10; Length 900; Similarity 99.8%; Pred. No. 8.5e-88; O; Conservative 0; Mismatches 1; Indels 0; Gaps AGTGGACGCCGAGGCCCGGAGTCGCGCCTGCAGACACAGCATCTACTCAGCGTGGGT 81	1:9606" 1:9606" 1996656" 1996656" 19 (phage-resistant)" 1 MGC 70" 1 MGC 70" 2 MGC 1 Vector: pCMV-SPORT6; Site 1: Not pancreas; Vectorionally. Primer: Oligo dT primer of the primer of t	Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9669 row: n column: 17 High quality sequence stop: 711. Location/Qualifiers 1980 /organism="Homo sapiens"	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 980) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: ggapbs-r@mail.nih.gov	BE904302 0 601494571F2 NIH_MGC_70 Homo sapiens cDNA clmRNA sequence. BE904302 BE904302.1 GI:10396415 EST. Homo sapiens (human) 4 Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Ver	GTAGTGGCATTCTATTTATTGTGACCTTTTCAATAAATAGATTTAAGTAAAAA 	AGCACTGTTTTTGTTTTAATGGTATATTTTTATTGGCTACTTTATTGTTTAGGACAAGTG	CCTCTGCCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTTTTT	GAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACGTCT	TGGCACAAAATCAGAGCAAGAAAGCGATGCCCTTCCCAATTCTCTCAATCCTTTTATGCC	

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordate; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 475)

NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Finis Clone is available royalty-free through LLNL; contact the
Insert Length: 1129
Std Error: 0.00
Seq primer: -40UP from Gibco
Seq primer: -40UP from Gibco
High quality sequence stop: 409.
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/lab host="PHIOB"
/lab host="PHIOB"
/clone lib="Soares WhHMPu S1"
/clone lib="Soare
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1879612"
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cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov d.column: 05
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 713)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                BI193763
BI193763.1 GI:14648783
                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                             602948418F1 NIH_MGC_42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.8%; Score 475; DB 9; 1
100.0%; Pred. No. 1.7e-86;
tive 0; Mismatches 0;
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Homo sapiens
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s cDNA clone IMAGE:5091412 5',
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δ В S 정 δ. 멼 Ş Db Ş 밁 Ś 밁 Ś В

High quality sequence stop: 709

JUNEAULED

Homo sapiens (human) Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

AW952776
EST364846 MAGE resequences, MAGE
AW952776

Homo **mRNA**

NA linear sapiens cDNA,

EST 01-JUN-2000 mRNA sequence.

EST AW952776.1

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Query Match
Best Local Similarity
Matches 514; Conserv
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                                                                                        GGACTTGCTGGGCCTTGGTGTGAGAGCAGGCATATTTGGAGGGGATCTGGTGGTGCCTTG
                   AAGGTATGATCAGAGAGAGGGGACCACAGGTGTGTGT 656
                                                                     GACTIGCTGGGCCTTGGTGTGAGAGCAGCATATTTGGAGGGATCTGGTGGTGCCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="epithelioid carcinoma cell line"
/lab host="DHIOB (phage-resistant)"
/clone_lib="NHI_MGC_42"
/clone_lib="NHI_MGC_42"
/note="Crgan: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: GCCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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/organism="Homo sapie:
/mol_type="mRNA"
/db_xref="taxon:9606"
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BG055477/c
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Best Local Similarity
Matches 455; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                       mRNA sequence.
BG055477
BG055477.1 GI:
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 446)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                          nad54h01.x1 NCI_CGAP_Lu24 Homo s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000) Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: johnq@tigr.org
Plate: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. Quackenbush,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACATGGGCTTTCCGCAGTGGCATCTCGGCAACCATGCTGTGGAGCCGGTGACCTCCATCC
                                                                                                                                                                                                                                                               TGCCCTTCCCAATTCTCTCAATCCTTTTATGCCGA 832
                                                                                                                                                                                                                                                                                                                                                                                     AGAGGGACTTGCTGGGCGTGTGAGAGCAGGCATATTTGGAGGGGATCTGGTGGTGC
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/db_xref="taxon:9606"
/clone lib="MAGE resequences, MAGE"
/note="Vector: pBluescriptSKm"
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                                                                                                         GI:12516626
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CDNA clone IMAGE:3407472 3',
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 438.
Location/Qualifiers
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                                                            GTGGTAGTGGCATTCTATTTATTGTG 1033
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/note="Organ: lung; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 141420-14179) and 1520904-1522439). Subtraction by Bento contents the same library (cloneIDs 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soares and M. Fatima Bonaldo.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 1.2e-80;
tive 0; Mismatches 0;
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Best Local &
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                                                                                                       237
81
                             297
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RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB NO.972)

http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101

Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 765)
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Human UnigeneSet - RZPD3
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BX095713 | 765 bp mRNA linear EST 04-FEB-2003
BX095713 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAG9998B081942 ; IMAGE:787879, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: CONTENT SEQUENCE: TTCACACAGGAAACAGCTATGAC.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RZPD Deutsches Ressourcenzentrum fuer Genomforschung
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                       Similarity 99.
93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Ina Rolfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX095713.1 GI:27842493
                                                                                             GAGGTAGCÀTTCCTCGACAGAGCTTCTTCAATAGGGGGCCATGGTGCTCCCCCAGGGGGTC 296
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                                                                                                                                                                      | CCAATGGGGAAATCGTGCAGGACGACGCCCCGGAGTGAGGGACCACTACCCAGCCACCAA 236
                                                                                                                                                                                                                            CAATTTCTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGTGCGGATCTTGG
                                                                                                                                                 CCAATGGGGAAATCGTGCAGGATGACGACCCCCGAGTGAGGACCACTACCCAGCCACCAA
                           CTGGCCCCCGCCAGCAGCAGGCAGGTGCCAGGCTGCTGCTCAGTCCCCCTTCAATG
                                                                    GAGGTAGCATTCCTCGACAGAGCTTCTTCAACAGGGGCCATGGTGCTCCCCCAGGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="IMAGD998B081942; IMAGB:787879"
/dev stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                       37.2%;
                                                                                                                                                                                                                                                                                                     Score 443; DB 13; Length 765; Pred. No. 2.8e-80; 0; Mismatches 3; Indels
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AUTHORS
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                                                                                                                                                                                                     375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soarse@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-35, pAT rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BU733254 19-OCT-2002
UI-E-CI1-afs-m-18-0-UI.s1 UI-E-CI1 Homo sapiens cDNA clone
UI-E-CI1-afs-m-18-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BU733254.1 GI:23659969
EST.
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97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            discovery
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/organism="HONO sapiens"
/mol type="mRNA"
/mol type="mRNA"
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/db xref="teaxon:9606"
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/dev stage="adltF
/dev stage="adltf fechnologies) (Tl phage resistant)"
/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
/clone_lib="UI-E-CII"
/clone_lib="UI-E-CII"
/clone_lib="UI-E-CII"
                                                                                                                                                                                             location/Qualifiers
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	following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA, synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTT3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute TAG_INSUE_RPE and Choroid TAG_LE=UI_E_CI1 TAG_SEQ=ACCTA"	
ORIGIN	H	
Query M Best Lo Matches	y Match 36.2%; Score 431; DB 13; Length 533; Local Similarity 99.6%; Pred. No. 1e-77; hes 531; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
\$ 8	544 GGGTGGGTTTGTTGAGAGGGACTTGCTGGGCCTTGGTGTGAGAGCAGGCATATTTGGAGG 603	
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DЪ	473 GGATCIGGTGGTGCTTGAAGGTATGATCAGAAGAGGGACCACAGGTGTGTGT	
γ	664 TIGIGITAAGCGIGAGGCAGAGGGAAGACGTTAGTCCAGCATTICCAAAGTGIGGGT 723	
Дb	413 TTGTGTTAAGCGTGAGGCAGAGGGAGGCGTTAGTCCAGCATTTCCAAAGTGTGGGTGG	
γQ	724 CCGTTGGTTCCCGAGATACTTTTAGGTGGTATTGGGGCCTGCATTAAGTGGCACAAAATCA 783	
Db	353 CCGTTGGTTCCCAAGATACTTTTAGGTGGTATGGGGCCTGCATTAAGTGGCACAAAATCA 294	
γQ	784 GAGCAAGAAAGCGATGCCCTTCCCCAATTCTCTCAATCCTTTTATGCCGAGAAGATCTCAG 843	
дb	293 GAGCAAGAAAGCGATGCCCTTCCCCAATTCTCTCAATCCTTTTATGCCGAGAAGATCTCAG 234	
Ş	844 CTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACGTCTCCTCTGCCTAGGG 903	
ф	233 CTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACGTCTCCTCTGCCTAGGG 174	
γQ	904 AGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGACTTTTTTTAGCACTGTTTTTG 963	
В	173 AGCAGGACTTGGGCTAGGGCAGGTGGAAAAAATTCCAGACTTTTTTTAGCACTGTTTTTTG 114	
Ş	964 TTTTAATGGTATATTTTTATTGGCTACTTTATTGTTTAGGACAAGTGGTAGTGGCAATTCT 1023	
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Search completed: August 22, 2004, 07:09:17 Job time : 3000 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 22, 2004, 04:42:00 ; Search time 117 Seconds (without alignments) 5653.859 Million cell updates/sec

Scoring table: Title: Perfect score: l aaaccgcctggagccgccgg.....gaagaggacacacggaaccc 1192 US-10-001-885-31 1192

OLIGO_NUC Gapop_60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:

1365418

Word size :

0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	BB	ij	Description
<u> </u>	792	66.4	1049	4	US-09-149-476-58	, **
N	473	39.7	483	4	98-9	equence 864,
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	31	2.6	396	4.	0-173-12	e 125
c 18	31	2.6	396	4.	US-09-713-550-125	e 125
 ப	31	2.6	469	w	1-43	e 436
N	31	2.6	569	w	US-09-328-111-561	e 56
21	31	2.6	958	N	US-08-757-046A-5	0 5
22	31		958	w	7-208-	e 5
23	31	2.6	958	w	US-09-135-988-5	~
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25	31		958	w	US-08-597-274A-5	5
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Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 37, Appli Sequence 4, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 3, Appli Sequence 201, App

ALIGNMENTS

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G DATE: 1997-05-23 CATION NUMBER: 60/047, G DATE: 1997-05-23 CATION NUMBER: 60/047, G DATE: 1997-05-23 CATION NUMBER: 60/047, G DATE: 1997-05-23 CATION NUMBER: 60/047, G DATE: 1997-05-23	DATE: 1997-05-23 UNION NUMBER: 60/047,5 UNION NUMBER: 60/047,6	1997-03-07 11997-03-07 11997-03-07 11997-03-07 11997-03-07 11997-03-07 11997-03-07 11997-03-07 11997-05-23 11997-05-23 11997-05-23	PZ002P1 TION NUMBER: US/09/149,476 DATE: 1998-09-08 NION NUMBER: PCT/US98/04493 DATE: 1998-03-06 DATE: 1997-03-07 NION NUMBER: 60/040,162 DATE: 1997-03-07 NION NUMBER: 60/040,333 DATE: 1997-03-07 NION NUMBER: 60/038,621 DATE: 1997-03-07 DATE: 1997-03-07 DATE: 1997-03-07 DATE: 1997-03-07 DATE: 1997-03-07 DATE: 1997-03-07 DATE: 1997-03-07	476-58 58, Application US/09149476 o. 6420526 INFORMATION: MT: Rosen et al. F INVENTION: 186 Human Secreted proteins

R FILING DATE R APPLICATION	ATION TION TION	LIER APPLICATION NUMBER: LIER APPLICATION NUMBER: LIER FILLING DATE: 1997-0. LIER FILLING DATE: 1997-0. LIER FILLING DATE: 1997-0. LIER APPLICATION NUMBER: LIER APPLICATION NUMBER: LIER APPLICATION NUMBER: LIER FILLING DATE: 1997-0.	APPLICATION FILING DATE
1,197-08-2; 1,197-08-2; 1,197-08-2; NUMBER: 60/056,882; 1,197-08-2; 1,197-08-2; 1,197-08-2; NUMBER: 60/056,637; 1,197-08-2; NUMBER: 60/056,903; 1,197-08-2; NUMBER: 60/056,888; 1,197-08-2; NUMBER: 60/056,888; 1,197-08-2; NUMBER: 60/056,889; 1,1997-08-2; NUMBER: 60/056,889; 1,1997-08-2; NUMBER: 60/056,889;	NUMBER: 60/043,672 : 1997-04-11 : 1997-04-11 : 1997-04-12 : 1997-04-13 : 1997-04-16 : 1997-08-22 : NUMBER: 60/056,886 : 1997-08-22 : NUMBER: 60/056,877 : 1997-08-22 : NUMBER: 60/056,893	NUMBER: 60/043,568 : 1997-04-11 NUMBER: 60/043,314 : 1997-04-11 NUMBER: 60/043,569 : 1997-04-11 NUMBER: 60/043,311 : 1997-04-11 NUMBER: 60/043,671 : 1997-04-11 NUMBER: 60/043,674 : 1997-04-11 NUMBER: 60/043,674 : 1997-04-11 NUMBER: 60/043,674 : 1997-04-11 NUMBER: 60/043,312 : 1997-04-11 NUMBER: 60/043,313	, H C B C B C B C B C B C B C B C B C B C
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ER FILLING DATE: 1997-09-05
ER FILLING DATE: 1997-06-10
ER FILLING DATE: 1997-06-13
ER APPLICATION NUMBER: 60/061,060
ER FILING DATE: 1997-10-02 406 301 346 241 286 181 121 106 361 226 586 481 526 421 466 781 824 721 764 661 705 601 646 541 46 61 μ CCCCTTCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCATCTCGG CAAGCCTCCCTCAATTTCTGGTGCAGCCCATCAGGGACCCACAGCGCCCTGGGAGGATGGT TGTTCGTGGCCTCCTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTG CAACCATGCTGTGGAGCCGGTGACCTCCATCCTGCTCCTCTTCCTGCTCATGATGCTTGG cccadederecredececedecadeadeadeadereceaderecrederecrederec CCAGCCACCAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCC CCAGCCACCAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCC GCGGATCTTGGCCAATGGGGAAAATCGTGCAGGACGACGACCCCCGAGTGAGGACCACTAC CAAGCCTCCCTCAATTTCTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGT TRATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCC CATTAAGTGGCACAAAATCAGAGCAAGAAAGCGATGCCCTTCCCAATTCTCTCAATCCTT CATTAAGTGGCACAAAATCAGAGCAAGAAAAGCGATGCCCTTCCCAATTCTCTCAATCCTT TTCCCAAAGTGTGGGTGGTTCCCGAGATACTTTTAGGTGGTATGGGGCCTG TT-CCAAAGTGTGGGTGGGTCCGTTGGTTCCCGAGATACTTTTAGGTGGTATGGGGCCTG | CAGGTGTGTGTTTCCCCTTTGTGTTAAGCGTGAGGCAGAGGGGAGACGTTAGT-CCAGCAT AGCAGGCATATTTGGAGGGGATCTGGTGGTGCCTTGAAGGTATGATCAGAGAGGGGACCA AGCAGGCATATTTGGAGGGGATCTGGTGGTGCTTGAAGGTATGATCAGAGAGGGGACCA ACCTCTGAGGGCTGATAGGGGTGGGTTTGTTGAGAGGGACTTGCTGGGCCTTGGTGAG ACCTCTGAGGGCTGATAGGGGTGGGTTTGTTGAGAGGGACTTGCTGGGCCTTGGTGTGAG CTTTTTAGCACTGTTTTTGTTTTAATGGTATATTTTTATTGGCTACTTTATTGTTTAGG 66.4%; nilarity 99.8%; Conservative 0; Score 792; DB Pred. No. 0; 0; Mismatches 멂 4; Length 1049; 0 2 120 165 60 180 225 465 360 405 300 240 285 600 585 480 525 420 660 704 645 540 943 840 883 823 720 763

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GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human P
FILE REFERENCE: GENSET 054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 864

LENGTH: 483

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAMP/KEY: CDS

LCCATION: 171..482

US-09-621-976-864
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100.0%; Pred. No. 9.6e-202;
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RESULT 3 US-09-621-976-3064

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GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dobert, S.
APPLICANT: Gobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3064
LENGTH: 519
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US-08-747-221B-24
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                                                    Sequence 24, Application US/08747221B Patent No. 6063610
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Best Local Similarity 99.6
Matches 235; Conservative
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APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
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LOCATION: 93..431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 80525
                                                                                                                                                                                                                                                                                                              ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 AGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCCCCCAGGGG 351
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                                                                                                                                                                                                                                                                                                   Colorado
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                                                      Matches
                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                  TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
            1052 ТТТААСТААААААААААААААААААААААААА
                                                    34;
                                                2.9%; Score 34; DB 3; Idiarity 100.0%; Pred. No. 7.4e-06; Conservative 0; Mismatches 0;
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STAILS:
COUNTRY: USA
ZIP: 80525
ZOWNOTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordberfect for Windows, Version 7.0
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/747, 221B
FILING DATE: NO.603610ember 12, 1996
ATTORNEY/AGENT IMFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-747-221B-26/C

; Sequence 26, Application US/08747221B

; Patent No. 6063610

; GENERAL INFORMATION:
                                                                       TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 2836 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2836 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 2.9%; Score 34; DB 3; L
Local Similarity 100.0%; Pred. No. 7.4e-06;
nes 34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 99..1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1052 ТТТААСТАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛ 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2778 ТТТААСТАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛ 2811
linear
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Length 2836;

0;

Gaps

0

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RESULT 6
US-09-005-051-24
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US-09-005-051-26/c
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                                                                                                                                                                   Sequence 26, Application US/09005051
Patent No. 6291222
                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
OPERATING SYSTEM: Windows, Version 7.0
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: FC-1 TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
APPLICATION NUMBER: 0291222ember 12, 1996
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NUMBE: VESSEY CASOL TAILSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2836 nucleotid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                             APPLICANT: Silver, Gary W. APPLICANT: Wisnewski, Nanc
TITLE OF INVENTION: No. 63
TITLE OF INVENTION: Molecu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Port Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                            ocal
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                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         h 2.9%;
Similarity 100.0%;
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Carol Talkington Verser, Ph.D
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                                                             ci, Nancy
No. 6291222el Carboxylesterase Nucleic Acid
Molecules, Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 3; Length 2836; Pred. No. 7.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: FC-1-C1-PUS
CURRENT APPLICATION NUMBER: US/09/403,942F
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: PCT/US97/20598
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-12
PRIOR PILING DATE: 1996-11-12
PRIOR FILING DATE: 1996-11-12
PRIOR FILING DATE: 1996-11-12
PRIOR FILING DATE: 1996-11-12
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Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 24
LENGTH: 2836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6664090 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS
SEQUENCE CHARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Silver, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: NOVEL CARBOXYLESTERASE NUCLBIC ACID MOLECULES, PROTEINS AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Brandt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                               LOCATION: (99)..(1889)
OTHER INFORMATION:
                                                                                                                                                                                                                         FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                              ORGANISM: Ctenocephalides felis
                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: FC-1 TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272
NAME/KEY: misc_feature
LOCATION: (2278)..(2278)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1052 TTTAAGTAAAAAAAAAAAAAAAAAAAAAAAAA 1085
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OTHER INFORMATION: n = unknown

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RESULT 10
US-09-621-976-17202
; Sequence 17202, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
                                                                                                            ; SOFTWARE: Patent.pm

; SEQ ID NO 17202

; LENGTH: 364

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-621-976-17202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature; LOCATION: (559)...(559)
; OTHER INFORMATION: n = unknown
US-09-403-942F-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-403-942F-26/c
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                       Query Match
Best Local Similarity 100.
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 2836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26, Application US/09403942F Patent No. 6664090 GENERAL INFORMATION:
                                                                                                                                                                                                                                  APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%; Score 34; DB 4; Louis Local Similarity 100.0%; Pred. No. 7.4e-06; Matches 34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: PCT/US97/20598
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 08/747,221
PRIOR FILING DATE: 1996-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Silver, Gary M.
APPLICANT: Brandt, Kevin S.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: NOVEL CARBOXYLESTERASE NUCLEIC ACID MOLECULES, PROTEINS AND USES
FILE REFERENCE: FC-1-C1-PUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/403,942F CURRENT FILING DATE: 2000-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Ctenocephalides felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1052 TTTAAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1085
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302 CCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 ТТТААСТАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.9%; Score 34; DB 4; Le ilarity 100.0%; Pred. No. 7.4e-06; Conservative 0; Mismatches 0;
                       2.7%; Score 32; DB 4; Length 364
100.0%; Pred. No. 6.1e-05;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2836;
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APPLICANT: Broad, Sean
APPLICANT: Pacper, Bryan
APPLICANT: Stachling-Hampton, Karen
APPLICANT: Stachling-Hampton, Karen
APPLICANT: Stachling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
FILE REFERENCE: 24003.51.5
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-08-368-776A-4
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US-09-918-686-7
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Best Local Similarity
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Patent No. 6475739
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
    APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                         SOFTMARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION STRATE
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                               PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                           FILING DATE: January CLASSIFICATION: 435
                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Application US/08368776A 6300482
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Millauer, Birgit
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AND TREATMENT OF MDK1
SIGNAL TRANSDUCTION
DISORDERS
                                                                                                                                               US/08/368,776A
Y 3, 1995
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                                                                 including application described below:
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GENERAL INFORMATION:
APPLICANT: Thomas Ciossek, Axel UI
APPLICANT: Millauer
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                              TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Ly
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CITY: Los Angeles
STATE: California
                                                                               TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: Januar CLASSIFICATION:
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Local Similarity
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                                                                                                                                                                                                    TELEPHONE: (213) 489-160
TELEPAX: (213) 955-0440
                                                                                                                                 LENGTH:
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Similarity 100.0%;
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                                                                TYPE:
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633 West Fifth Street
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                                                                  nucleic
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                                                                                                                                                                                                                      489-1600
2.7%;
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Y 3, 1995
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DB 5; L
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GENERAL INFORMALLANT,
APPLICANT: Brunkow, Mary
APPLICANT: Proll, Sean
APPLICANT: Paeper, Bryan
APPLICANT: Staehling-Hampton, K
ADDLICANT: Staehling-Hampton, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ś
                                                                                ; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 7043, 8369, 8401
; OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1
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Query Match
Best Local Similarity 100.
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1246, 2572, 2604
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                   SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                      APPLICANT: Brunkow, Mary
APPLICANT: Proll, Sean
APPLICANT: Paeper, Bryan
APPLICANT: Staehling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REFERENCE: 240083.515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS FOR IDENTI
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REFERENCE: 240083.515
                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                      TYPE: DNA
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). 6475739
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il Similarity 100.0%;
32; Conservative
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       2.7%; 500
100.0%; Pr
                              Score 32; DB 4; L; Pred. No. 5.2e-05;
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Pred. No.
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                Mismatches
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                                             Length 92139;
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1055 ААСТАААЛАЛЛААЛААЛААЛААЛААЛАЛАА

Search completed: August 22, 2004, 07:11:24 Job time : 119 secs 50660 PAGENARARARARARARARARARARARARARA 50691

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Regult
No.
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Maximum DB seq length: 2000000000
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GENERAL INFORMATION:

Sequence 31, Application US/10001885 Publication No. US20040058319A1

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APPLICANT: Macina, Roberto
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APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
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NUMBER OF SEQ ID NOS: 167
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PRIOR APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOPTWARE: PatentIn Ver. 3.1
SEQ ID NO 619
LENGTH: 1108
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1101)
OTHER INFORMATION: n equals a,t,9, or c
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Publication No. US20040009491A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
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	226 CCAGCCACCAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGGCCATGGTGCTCC 285	Ś
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	46 TCGCGCCTGCAGACACAGCATCTACTCAGCGTGGGTCACCTCTGTGAACATCACTGACTG	Ś
	Query Match 66.4%; Score 792; DB 10; Length 1049; Best Local Similarity 99.8%; Pred. No. 0; Matches 1032; Conservative 0; Mismatches 0; Indels 2; Gaps 2;	Qu Ma
	ORGANISM: Homo sapiens 9-809-391-58	US-0
	LENGTH: 1049 TYPE: DNA	·- ·- ·
	OFTWARE: PatentIn Ver. 2.0	 S S
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	URRENT APPLICATION NUMBER: US/09/809,391	
	APPLICANT: KUDEN et al. TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: PZ002P2	 va⊢1≱
	blication No. US20030049618A1 NERAL INFORMATION:	GE ;
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-	968 ATTGGCTACTTTATTGTTTAGGACAAGTGGTAGTGGCATTCTATTTATT	dg d
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RESULT 4
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US-09-882-171-58
; Sequence 58, Application US/09882171
; Publication No. US20030175858A1
; Publication No. US20030175858A1
; GENERAL INFORMATION;
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/882,171
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR APPLICATION NUMBER: 09/040,162
; PRIOR FILING DATE: 1998-03-06
; PRIOR FILING DATE: 1998-03-07
; PRIOR FILING DATE: 1997-03-07

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R FIL R APP	20 20		PRIOR FILING DATE: 1997-05	FRIOR FEILING DATE: PRIOR PRIOR FILING DATE: PRIOR APPLICATION NUMBER:	; PRIOR APPLICATION NUMBERS ; PRIOR	; PRIOR APPLICATION NUMBER: ; PRIOR FILING DATE: 1997-05	; PRIOR APPLICATION NUMBER: ; PRIOR FILING DATE: 1997-08	PRIOR FILING DATE: 1997-08	PRIOR FILING DATE: 1997-08	PRIOR FILING DATE: 1997-08	PRIOR FILING DATE: 1997-08 PRIOR APPLICATION NUMBER:	; PRIOR FILING DATE: 1997-08 ; PRIOR APPLICATION NUMBER:	; PRIOR APPLICATION NUMBER:	, FRICK APPLICATION NUMBER:	PRIOR APPLICATION NUMBER:	PRIOR APPLICATION NUMBER:				; PRIOR FILING DATE: 1997-09; PRIOR APPLICATION NUMBER: 1007-09	; PRIOR FILING DATE: 1997-08	; PRIOR FILING DATE: 1997-08; PRIOR APPLICATION NUMBER:	; PRIOR FILING DATE: 1997-08 ; PRIOR APPLICATION NUMBER:	PRIOR FILING DATE: 1997-08 PRIOR APPLICATION NUMBER:	PRIOR FILING DATE: 1997-08	PRIOR FILING DATE: 1997-08 PRIOR APPLICATION NUMBER:	PRIOR FILING DATE: 1997-08	PRIOR FILING DATE: 1997-08	PRIOR FILING DATE: 1997-08					
R FIL R APP	20 20		PRIOR FILING DATE: 1997-05-23	FRICE REFLICATION NUMBER: 60/04 PRIOR BELICATION NUMBER: 60/04	; PRIOR APPLICATION NUMBER: 60/04 ; PRIOR FILING DATE: 1985EX: 65/04	; PRICK APPLICATION NUMBER: 60/04; PRICK FILING DATE: 1997-05-23; PRICK FILING DATE: 1997-05-23	; PRIOR APPLICATION NUMBER: 60/05 ; PRIOR FILING DATE: 1997-08-22 ; PRIOR FILING DATE: 1997-08-22	PRIOR FILING DATE: 1997-08-22	PRIOR FILING DATE: 1997-08-22	PRIOR FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: 60/05	; PRIOR FILING DATE: 1997-08-22 ; PRIOR APPLICATION NUMBER: 60/05	; PRIOR FILING DATE: 1997-08-22; ; PRIOR APPLICATION NUMBER: 60/05;	; PRIOR APPLICATION NUMBER: 60/05	PRIOR PERIOR NUMBER: 60/05	PRIOR ETITIO DATE: 1002-06-22	PRIOR ETITING DATE: 1997-08-22				; PRIOR FILING DATE: 1997-08-22 ; PRIOR PEPLICATION NUMBER: 60/05 ; PRIOR APPLICATION NUMBER: 60/05	; PRIOR FILING DATE: 1997-08-22 ; PRIOR APPLICATION NUMBER: 60/05	; PRIOR FILING DATE: 1997-08-22 ; PRIOR APPLICATION NUMBER: 60/05	; PRIOR FILING DATE: 1997-08-22 ; PRIOR APPLICATION NUMBER: 60/05	PRIOR FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: 60/05	PRIOR FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: 60/05	FRIOR FILING DATE: 1997-08-22 FRIOR APPLICATION NUMBER: 60/05	PRIOR FILING DATE: 1997-08-22	PRIOR FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: 60/05	PRIOR FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: 60/05					
R FILING DATE: 1997-05- R APPLICATION NUMBER: 6	20 20	PRIOR FILING DATE: 1997-05-23 PRIOR APPLICATION NUMBER: 60/047,590	PRIOR EILING DATE: 1997-05-23	FRICK AFFELCATION NUMBER: 60/047,585	; PRIOR APPLICATION NUMBER: 60/047,599 ; PRIOR FILING DATE: 1985K: 60/047,588	; PRIOR APPLICATION NUMBER: 60/04/,595 ; PRIOR FILING DATE: 1997-05-23	; PRICE APPLICATION NUMBER: 60/057,761 ; PRICE FILING DATE: 1997-08-22	PRIOR FILING DATE: 1997-08-22	; PRIOR FILING CALC. 1997-08-22	PRIOR FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: 60/056,845	; PRIOR FILING DATE: 1997-08-22 ; PRIOR APPLICATION NUMBER: 60/056,631	; PRIOR FILING DATE: 1997-08-22 ; PRIOR APPLICATION NUMBER: 60/056,864	; PRIOR APPLICATION NUMBER: 60/056,910	; PRIOR PRILICATION NUMBER: 60/056,874	FRANCE REPLIES TO THE TOTAL TOT	PRIOR PELICATION NUMBER: 60/056,911			FRIOR FILING TARE: 1307-00-22 FRIOR PERIOR PERIOR TO TARE: 1807-06-22	; FRICK FILING DATE: 1997-08-22 ; PRICK PEPLICATION UNUBER: 60/056,888 parch prick Date: 1007-08-22	; PRIOR FILING DATE: 1997-08-22; PRIOR APPLICATION NUMBER: 60/056,903	; PRIOR FILING DATE: 1997-08-22 ; PRIOR APPLICATION NUMBER: 60/056,637	; PRIOR FILING DATE: 1997-08-22 ; PRIOR APPLICATION NUMBER: 60/056,882	PRIOR FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: 60/056,872	PRIOR FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: 60/056,662	PRIOR PRINTED DATE: 1997-08-28 PRIOR APPLICATION NUMBER: 60/056,878	PRIOR FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: 60/056.630	PRIOR FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: 60/056,893	FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056			FRIOR REPLICATION NUMBER: 60/048,974 PRIOR APPLICATION NUMBER: 60/048,974		; PRIOR FILING DATE: 1997-04-11; PRIOR APPLICATION NUMBER: 60/043,313; PRIOR FILING DATE: 1997-04-11; PRIOR FILING DATE: 1997-04-11

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Best Local Similarity
Matches 1032; Conserv PRIOR IOR APPLICATION NUMBER: 60/047,593
IOR FILING DATE: 1997-05-23
IOR APPLICATION NUMBER: 60/047,614
IOR FILING DATE: 1997-05-23
IOR APPLICATION NUMBER: 60/043,578
IOR APPLICATION NUMBER: 60/043,576
IOR FILING DATE: 1997-04-11
IOR APPLICATION NUMBER: 60/047,501
IOR APPLICATION NUMBER: 60/047,501
IOR APPLICATION NUMBER: 60/047,501
IOR APPLICATION NUMBER: 60/047,670
IOR FILING DATE: 1997-04-11
IOR APPLICATION NUMBER: 60/056,632
IOR FILING DATE: 1997-08-22
IOR FILING DATE: 1997-08-22
IOR APPLICATION NUMBER: 60/056,664
IOR FILING DATE: 1997-08-22
IOR APPLICATION NUMBER: 60/056,664
IOR FILING DATE: 1997-08-22
IOR APPLICATION NUMBER: 60/056,664
IOR FILING DATE: 1997-08-22
IOR APPLICATION NUMBER: 60/056,876
IOR APPLICATION NUMBER: 60/056,876 CR APPLICATION NUMBER: 60/056,881

OR FILING DATE: 1997-08-22

OR APPLICATION NUMBER: 60/056,909

OR FILING DATE: 1997-08-22

OR APPLICATION NUMBER: 60/056,875

OR APPLICATION NUMBER: 60/056,862

OR FILING DATE: 1997-08-22

OR APPLICATION NUMBER: 60/056,862

OR FILING DATE: 1997-08-22

OR APPLICATION NUMBER: 60/056,887

OR APPLICATION NUMBER: 60/056,908

OR APPLICATION NUMBER: 60/056,908

OR APPLICATION NUMBER: 60/057,650

OR FILING DATE: 1997-06-06

OR FILING DATE: 1997-08-28

OR FILING DATE: 1997-09-05

OR FILING DATE: 1997-09-05

OR APPLICATION NUMBER: 60/057,669

OR APPLICATION NUMBER: 60/057,669 301 121 241 286 181 226 166 106 466 361 406 346 61 46 CCAGCCACCAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCC GCGGATCTTGGCCAATGGGGAAAATCGTGCAGGACGACGACCCCCGGAGTGAGGACCACTAC CAAGCCTCCCTCAATTTCTGGTGCAGCCCATCAGGGACCCACAGCGCCTGGGAGGATGGT CAAGCCTCCCTCAATTTCTGGTGCAGCCCATCAGGGACCCACAGCGCCCTGGGAGGATGGT rededecrigeadacacadeareraereaecidegereaecrerereaeaecaceaecre CAACCATGCTGTGGAGCCGGTGACCTCCATCCTGCTCCTCTTCCTGCTCATGATGCTTGG CCCCTTCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTTCCGCAGTGGCATCTCGG | CCCAGGGGGTCCTGGCCCCGCCAGCAGCAGCAGGCAGGTGCCAGGCTGGGTGCTCAGTC CCAGCCACCAAGAGATAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGTGCTCC TGTTCGTGGCCTCCTCGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTG CCCCTTCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCATCTCGG Conservative 99.88; Score 792; DB Pred. No. 0; 0; Mismatches DB 10; 0, Length 1049; Indels 22 180 225 165 60 105 525 465 360 405 300 345 240 285 120 420

CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
PRIOR FILING DATE: 1998-3-06
NUMBER OF SEQ ID NOS: 757
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58
LENGTH: 1049 Ş 8 밁 S 문 8 밁 S S 8 片 Ś 맑 3 밁 片 RESULT 5 US-10-164-861-58 片 δ 밁 밁 ; TYPE: DNA; ORGANISM: Homo sapiens US-10-164-861-58 닭 Ş Sequence 58, Application US/10164861
Publication No. US20030225248A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1 Query Match Best Local Similarity Matches 1032; Conserv 1021 1064 1004 421 541 586 481 901 661 601 646 196 944 841 884 781 824 721 764 705 ACCTCTGAGGGCTGATAGGGGTGGGGTTTGTTGAGAGGGACTTGCTGGGCCTTGGTGTAG CATTAAGTGGCACAAAATCAGAGCAAGAAAGCGATGCCCTTCCCAATTCTCTCAATCCTT caggrerererricecerriererraagegreagegagagagagagerragreecagear CAGGTGTGTGTTTCCCCTTTGTGTTAAGCGTGAGGCAGAGGGAGACGTTAGT-CCAGCAT TGTTCGTGGCCTCCTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAGCGGTG 480 CATTAAGTGGCACAAAATCAGAGCAAGAAAAGCGATGCCCTTCCCCAATTCTCTCAATCCTT TT-CCAAAGTGTGGGTGGGTCCGTTGGTTCCCGAGATACTTTTAGGTGGTAIGGGGCCTG AGCAGGCATATTTGGAGGGGATCTGGTGGTGCCTTGAAGGTATGATCAGAGAGGGGGACCA ACCTCTGAGGGCTGATAGGGGTGGGTTTGTTGAGAGGGACTTGCTGGGCCTTGGTGTGAG AAAAAAAAAAAA 1034 AAAAAAAAAAAA 1077 CTTTTTAGCACTGTTTTTGTTTTAATGGTATATTTTTATTGGCTACTTTATTGTTTAGG CTTTTTAGCACTGTTTTGTTTTAATGGTATATTTTATTGGCTACTTTATTGTTTAGG GACGTCTCCTCTGCCTAGGGAGCAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTCCAGA GACGTCTCCTTGCCTAGGGAGGAGGACTTGGGCTTAGGGCAGGTGGAAAAAATTTCCAGA 943 TTATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCC TTATGCCGAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCC rrcccaaagreregeregerecerregreedagaracrrrageregraregere Application US/10164861 Conservative 66.4%; 99.8%; Score 792; DB Pred. No. 0; O Mismatches 0; DB 0 Length Indels <u>ب</u> Gaps 645 540 900 840 823 660 704 600 585 1020 1063 960 1003 883 720 763 60 105

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APPLICANT: Tang, Y. Tom

APPLICANT: Xue, Aidong J.

APPLICANT: Lower Anadje T.

APPLICANT: Drmanac, Raddje T.

TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Prot

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 803 1CNCP

CURRENT APPLICATION NUMBER: US/10/302,172

CURRENT FILING DATE: 2002-01-21

PRIOR APPLICATION NUMBER: US 10/225,251

PRIOR FILING DATE: 2002-08-20

PRIOR FILING DATE: 2002-03-05

PRIOR FILING DATE: 2002-03-05

PRIOR FILING DATE: 2002-03-05

PRIOR FILING DATE: 2002-03-05

PRIOR FILING DATE: 2001-03-05

VOUMBER OF SEQ ID NOS: 950

SOFTWARE: pt FL genes Version 2.0

SEQ ID NO 94

LENGTH: 1052

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (365)..(508)

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; ORGANISM: Homo sapien
US-10-076-747-65
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GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 65
LENGTH: 365
                                                                                                     Sequence 64, Application US/10076747
Publication No. US20030180726A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 65, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.3%; Score 326; DB 15; Length 365; Best Local Similarity 100.0%; Pred. No. 1.1e-155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/266,290
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: 60/268,834
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 129
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and FILE REFERENCE: DEX-0315
CURRENT APPLICATION NUMBER: US/10/076,747
CURRENT FILING DATE: 2002-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Recipon, Herve
APPLICANT: Karra, Kalpana
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
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APPLICANT: Recipon, Herve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 GACGACCCCGAGTGAGGACCACTACCCAGCCACCAAGAGGTAGCATTCCTCGACAGAGC 99
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                                                                                                                                                                                                                                                                               CTGGTGTCCCACCTGAGTCAGCGGTG 525
                                                                                                                                                                                                                                                                                                                               CTCCTCTTCCTGCTCATGATGCTT
                                                                                                                                                                                                                                                                                                                                                                        CTCCTCTTCCTGCTCATGATGCTTGGTGTTCGTGGCCTCCTCCTGGTTGGCCTTGTCTAC 499
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No. US20030180726A1
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828 GCCGAGAAGATCTCAGCTGGATGCCAACATGTTCCGATGCCTGTGGAAGACATGCCGACG 887

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; TYPE: DNA; Homo sapien US-10-076-747-64
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                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-885-30
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US-10-001-885-30
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                                                                                                                                           APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and I
FILE REFERENCE: DEX-0279
CURRENT APPLICATION NUMBER: US/10/001,885
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,061
PRIOR APPLICATION NUMBER: 60/252,061
PRIOR APPLICATION NUMBER: 60/253,257
PRIOR APPLICATION NUMBER: 60/253,257
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 167
SEQ ID NO 30
LENGTH: 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30, Applica Publication No. US20 GENERAL INFORMATION:
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Best Local Similarity
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Matches 125;
                    Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/076,747
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/268,290
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: 60/268,834
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 129
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APPLICANT: Macina,
APPLICANT: Recipon,
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Cafferkey, Robert
Sun, Yongming
Liu, Chenghua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macina, Roberto
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lo. US20040058319A1
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  Conservative
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100.0%; Pred. No. 8.1e-89;
tive 0; Mismatches 0;
10.5%; Score 125; DB 13; 100.0%; Pred. NO. 4.4e-53; ... Mismatches 0;
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                                         Length 643;
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  Indels · 0;
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US-09-864-761-5591
US-09-864-761-5591, Application US/09864761
Sequence 5591, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng;
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL:
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Accomica-X-1
FILE REFERENCE: Accomica-X-1
FILE REFERENCE: Accomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-03
PRIOR PRILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00665
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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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                                                                                                      PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 5591
SEG ID NO 5591
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
FEATURE:
CTHER INFORMATION: MAP TO ACCO4514.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
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US-09-864-761-5591
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Best Local
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APPLICANT: Rank, David I
APPLICANT: Hanzel, David
TYPE: DNA
ORGANISM: Homo
sapiens
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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
OTHER INFORMATION: APPLICANT HELA, SIGNAL = 3.5
OTHER INFORMATION: HELA, SIGNAL = 3.5
OTHER INFORMATION: HEART ANALAMANA, SIGNAL = 3.6
OTHER INFORMATION: HEART ANALAMANA, SIGNAL = 3.6
OTHER INFORMATION: HEART ANALAMANA, SIGNAL = 3.5
OTHER INFORMATION: HEART A
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APPLICATION: THINGS OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY ON: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR THILE OF INVENTION: GREE EXPRESSION ANALYSIS BY MICROARRAY

PILE REFERENCE: ABONIGS -X-1

CURRENT PILLY DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-01-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00666

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US-10-027-632-209023
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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Sequence 209023, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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SEQ ID NO 209023
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Publication No. US20020198371A1
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION: MAP TO ACO04514.1

INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6

INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4

INFORMATION: EXPRESSED IN BARIN, SIGNAL = 1.8

INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7

INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
                                                                                                                                                                                                                                                                                                                                                         307 ТАСАТТТААСТАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 ТАСАТТТААСТААААААААААААААААААААААА
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nilarity 100.0%;
Conservative (
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; Pred. No. 1.1e-08;
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FUDILICALY: SILVER, GARY M.
APPLICANT: Silver, Gary M.
APPLICANT: Brandt, Kevin S.
APPLICANT: Wisnewski, Nancy
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: MOYEL CARBOXYLESTERASE NUCLEIC ACID MOLECULES, PROTEINS AND USES
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; ORGANISM: Human
US-10-027-632-209023
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 125925
LENGTH: 616
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 125925, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 209023
LENGTH: 998
                                                                                                                                                                                                           Sequence 24, Application US/10678521 Publication No. US20040081998A1
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Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-028
PRIOR FILING DATE: 1999-028
PRIOR APPLICATION NUMBER: US 60/146,002
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APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILLING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILLING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: PAT_MRT3847_84719C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine max FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    34; Conservative
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Pred. No. 1.2e-0
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CURRENT APPLICATION NUMBER: US/10/678,521

CURRENT FILING DATE: 2003-10-02

PRIOR APPLICATION NUMBER: US/09/403,942F

PRIOR APPLICATION NUMBER: US/09/403,942F

PRIOR APPLICATION NUMBER: COT/US97/20598

PRIOR APPLICATION NUMBER: 08/747,221

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 08/747,221

PRIOR FILING DATE: 1997-11-12

RIPATOR FILING DATE: 1996-11-12

RIPATOR FILING DATE: 1996-11-12

RIPATOR FILING DATE: 1996-11-12

RIPATOR: Patentin version 3.1

SEQ ID NO 24

LENGTH: 2836

TYPE: DNA

CRGANISM: Ctenocephalides felis

FEATURE:

NAME/KEY: CDS

COCATION: (2978). (1889)

COTHER INFORMATION: n = unknown

US-10-678-521-24

Query Match

Best Local Similarity 100.0%; Pred. No. 1.2e-06;

Matches 34; Conservative 0; Mismatches 0; Gaps

Office Indels 0; Gaps

Off
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0;

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd

OM protein - protein search, using sw model

August 24, 2004, 09:17:04; Search time 54 Seconds (without alignments) 633.116 Million cell updates/sec

Perfect score: Title: US-10-001-885-125 632

Sequence:

BLOSUM62

1 MVRILANGEIVQDDDPRVRT......GVRGLLLVGLVYLVSHLSQR 121

Scoring table:

Searched: 1586107 seqs, 282547505 residues Gapop 10.0 , Gapext 0.5

Minimum DB Maximum DB seq geq length: 0 length: 2000000000

Total number of hits satisfying chosen parameters:

1586107

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:* geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:* geneseqp2001s:*
geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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				21	20	19	18	17	16	15	14	13	12	11	10	ø	œ	7	9	IJ	4	ω	N	1	ŏ.	Result
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AAB93546	ABP52104	AAY71059	AAB12139	ADC33068	ABG14288	AAU68560	ABG03109	AAR27493	AAW41419	AAB42404	AAG77595	ADE08064	ABB84669	ABG00633	AB034421	ABG95227	ABP68995	AAW74777	AB034727	ABG95533	ADE60339	ADE60341	ABU61063	ABB79328	ID	
Huma	Abp52104 Homo sapi	Aay71059 Human mem	Aab12139 Hydrophob	œ	Abg14288 Novel hum	Aau68560 Human nov	φ		Aaw41419 Paxillin	4 Humar	Aag77595 Human col	Ade08064 Novel pro	Abb84669 Human SEC	Abg00633 Novel hum	Abo34421 Region of	Human	Abp68995 Human pol	Aaw74777 Human sec	Abo34727 Fragment	Abg95533 Human nov	Ade60339 Rat Prote	Ade60341 Rat Prote	Abu61063 Human ova	Abb79328 Human ova	Description	

4 5	44	43	42	44	40	39	38	37	36	35	34	33	32	31	'30	29	28	27	26
70	70	70	70	70	70.5	70.5	. 71	71	71	71	71	71	71.5	71.5	72	72.5	73	73	73.5
11.1	11.1	11.1	11.1	11.1	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.3	11.3	11.4	11.5	11.6	11.6	11.6
1128	387	379	266	213	915	226	1697	1030	689	349	345	124	19938	158	310	315	793	763	442
4	4.	7	4	Ø	თ	w	7	4	N	4.	w	4.	o	w	N	4	w	w	4.
ABB58911	ABG11608	ADB85283	ABG18528	ABP73050	ABP63120	AAB42794	ADC37542	ABG23699	AAW72025	ABG04137	AAY93600	AA001631	ABP76680	AAG22606	AAR23996	ABB61702	AAG42391	AAG42392	ABG09021
Abb58911	Abg11608	Adb85283	Abg18528	Abp73050	Abp63120	Aab42794	Adc37542	Abg23699	Aaw72025	Abg04137	Aay93600	Aac01631	Abp76680	Aag22606	Aar23996	Abb61702	Aag42391	Aag42392	Abg09021
Drosophil	Novel hum	Rat fooce	Novel hum	Amino	FLO11	Human	Human nuc	Novel hum	HSV-2 str	Novel hum	_	Human pol	_					-	Novel hum

ALIGNMENTS

RESULT 1 ABB79328

ABB79328 standard; protein; 121 AA.

ABB79328;

12-AUG-2002 (first entry)

Human ovary specific protein SEQ ID NO:125

Human; ovary specific nucleic acid; OSNA; ovary specific protein; OSP; ovary specific gene; OSG; ovarian cancer; immune response; metastasis.

Homo sapiens.

WO200240535-A2.

23-MAY-2002.

20-NOV-2001; 2001WO-US045011.

20-NOV-2000; 2000US-0252061P. 27-NOV-2000; 2000US-0253257P.

(DIAD-) DIADEXUS INC.

Salceda S, Macina RA, Recipon H, Cafferkey R, aus Ķ Liu

Ç

WPI; 2002-471617/50.

New ovary specific genes and proteins, useful as a vaccine for treating patients with ovarian cancer, or for diagnosing and monitoring the presence and metastases of ovarian cancer in a patient.

Claim 11; Page 241; 260pp; English.

ABN87790 to ABN87882 represent human ovary specific nucleic acid (OSNA) sequences, and ABB79297 to ABB79370 represent ovary specific protein (OSP) sequences from the present invention. OSNA and OSP sequences have cytostatic activity, and can be used in vaccine production and gene therapy. An antibody that specifically binds to an OSP can be used for treating a patient with ovarian cancer, particularly for inducing an immune response against the ovarian cancer cell expressing the OSNA or OSP. The OSNAs and OSPs can also be used for diagnosing and monitoring the presence and metastases of ovarian cancer in a patient

Sequence 121 AA;

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RESULT 2
ABUG1063
ID ABUG
XX ABUG
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XX ABUG
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Best Local Similarity
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                                                                           The invention relates to a new isolated nucleic acid termed ovarian specific nucleic acid (OSNA) comprising: (a) a nucleic acid molecule that encodes any of 53 fully defined protein sequences appearing as ABU61018-ABU61070 (termed ovarian specific proteins, OSP); (b) any of 76 fully defined nucleotide sequences appearing as ABS92187-ABS92262; or (c) a sequence having at least 60% sequence identity to the nucleic acid molecule of (a) or (b). Also included are a method for determining the presence of an ovary specific nucleic acid (OSNA) in a sample, a vector comprising an OSNA, a host cell comprising the vector, an isolated OSP polypeptide, an anti-OSP antibody or fragment, a method for determining the presence of an ovary specific protein in a sample and a vaccine comprising an OSP or OSNA. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous disease in ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated OSNA nucleic acid and encoded polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous diseases in ovarian tissues.
                                                tissue. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 220-221; 224pp; English.
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N-PSDB; ABX92251.
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Sun Y, Liu C;
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15-FEB-2001; 2001US-0268834P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ovarian specific protein DEX0310_122.
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Sequence 121 AA;

The invention discloses a composition comprising two or more isolated rat cor human polynucleotides or a polynucleotide which represents a fragment, consider the constructive or allelic variation of the nucleic acid sequence. Also comprising the vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a compound that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal contracted to pain, a method for identifying an agent compound which regulates the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal compound that is differentially expressed in neuronal tissue of a first animal compound that regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the contributy in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating the specification, a method for identifying a compound useful in treating the specification, a method for identifying a compound useful in treating the specification, a method for identifying a compound useful in treating the specification, a method for identifying a compound useful in treating the specification, a method for identifying a compound useful in treating the specification, a method for identifying a compound useful in treating the specification, a method for identifying a compound useful in treating the specification, a method for identifying a compound useful in treating the specification, a method for identifying a compound useful useful in treating the specification.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus.
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                                                                                                                                                                                                                                                                                                                                                                                                              Rat Protein
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Local Similarity 100.0%;
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Pred. No. 8.9e-62;
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Best Local
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 The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat Protein BAB25613, SEQ ID NO 6245
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                                                                                                          New composition comprising preparing a medicament for
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                                                                                                       two or more isolated polypeptides, useful treating pain in an animal.
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Pred. No. 9.1e
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                                07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn; nervous system disorder; Alzheimer's disease; infection; coular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive;
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                                                                                                                                                                                                                                                                                                                                                                                                           nutritional.
                                   97US-0038621P.
97US-0040161P.
97US-0040162P.
                                                                                                                                                            98US-00149476.
      97US-0040163P
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Pred. No. 9.
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                                                                                                                                                                                       CC The invention relates to an isolated protein that is one of 186 human CC secreted proteins, given in the specification, encoded by one of 309 cDNA CC sequences also given in the specification. The protein is used in a CC pharmaceutical composition used to prevent, treat or ameliorate a medical C condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, CC chickens or sheep. Disorders which are diagnosed or treated include CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative C disorders e.g. neoplasms of the breast or liver, cardiovascular disorders CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, CC angiogenesis, nervous system disorders e.g. Alzheimer's disease, CC infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound CC healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell CC culture of primary tissues, to regenerate tissues and in chemotaxis. The CC increase or decreese storage capabilities, fat content, lipid, protein, CC carbohydrate, vitamins, minerals, cofactors and other nutritional CC components. The present sequence represents one of the novel human CC secreted proteins of the invention
                                                                                                                     Query Match
Best Local S
Matches 73
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22-AUG-1997;
05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
12-SEP-1997;
02-OCT-1997;
06-MAR-1998;
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22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                       Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC; Bedharik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner I Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 50; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                     61
                                                     39
                                                                     1 MVRILANGEIVQDDDPRVRTTTQPPRGSIPRQSFFNRGHGAPPGGPGPRQQQAGARLGAA
                                                                                                                                     Similarity
QSPFNDLNRQLVN
                                                     MVRILANGEIVQDDDPRVRTTTQPPRGSIPRQSFFNRGHGAPPGGPGPRQQQAGARLGAA
                                                                                                                61.2%; Score 387; DB 5; I
Ilarity 100.0%; Pred. No. 9.5e-35;
Conservative 0; Mismatches 0;
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97US-0056911P.
97US-0057650P.
97US-0057669P.
97US-0057761P.
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97US-0056893P.
97US-0056894P.
97US-0056903P.
97US-0056908P.
97US-0056909P.
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97US-0061060P.
98WO-US004493.
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97US-0056879P
97US-0056880P
97US-0056881P
97US-0056884P
97US-0056884P
97US-0056886P
97US-0056888P
97US-0056888P
                     73
                                                                                                                                                     Length 111;
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, Brewer LA;
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970S-0047492P 970S-0047501P 970S-0047501P 970S-0047581P 970S-0047583P 970S-0047588P 970S-0047588P 970S-0047589P 970S-0047590P 970S-0047592P 970S-0047599P 970S-004759P 970S-004759P 970S-004759P 970S-004759P 970S-004761P 970S-005683P 970S-005683P 970S-005684P 970S-005687P 970S-005687P 970S-005687P 970S-005687P 970S-005687P 970S-005687P

23-MAY-1997; 23-MAY-1997; 23-MAY-1997; 23-MAY-1997; 23-MAY-1997;

11-APR-1997

97US-0043671P. 97US-0043672P. 97US-0043674P.

11-APR-1997

97US-0043313P 97US-0043314P 97US-0043315P 97US-0043568P 97US-00435769P 97US-0043578P 97US-0043578P 97US-004369P 97US-004369P 97US-0043669P

11-APR-1997

97US-0040333P. 97US-0040334P. 97US-0040336P.

23-MAY 1997;
24-AUG-1997;
25-AUG-1997;

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RESULT 6
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(Who breast cancer; wound; reproductive disorder; blood-related disorder;

(What haemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia;

(Whott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;

(Whypoplasia; wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;

(Whott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;

(Whott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;

(Whott-Aldrich syndrome; autoimmune disorder; allergy; asthma;

(Whott-Aldrich syndrome; autoimmune disorder; cytostatic;

(Whott-Aldrich syndrome; cardiama; congenital heart defect;

(Whott-Aldrich syndrome; neurological disorder; Alzheimer's disease;

(Whott-Aldrich syndrome; antibacterial; haemostatic; thrombolytic;

(Whott-Aldrich syndrome; sittlements; virucide; funglacide; anti-HIV; nephrotropic; antianginal;

(Whott-Aldrich syndrome; cardiant; nootropic; antiparkinsonian;

(Whott-Aldrich syndrome; has been syndrome; antianginal;

(Whott-Aldrich syndrome; autoimmune disorder; antianginal;

(Whott-Aldrich syndrome; autoimmune syndrome; antianginal;

(Whott-Aldrich syndrome; autoimmune disorder; antianginal;

(Whott-Aldrich syndrome; autoimmune syndrome; antianginal;

(Whott-Aldrich syndrome; autoimmune syndrome; antianginal;

(Whott-Aldrich syndrome; autoimmune syndrome; antianginal;

(Whott-Aldrich syndrome; antianginal;

(Whott-Aldrich syndrome; autoimmune syndrome; antianginal;

(Whott-Aldrich syndrome; autoimmune syndrome; antianginal;

(Whott-Aldrich syndrome; autoimmune syndrome; autoimmune syndrome; autoimmune syndrome; autoimmune syndrome; autoimmune syn
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07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
11-APR-1997;
11-APR-1997;
11-APR-1997;
11 APR 1997

23 -MAY 1997
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07-MAR-1997;
07-MAR-1997;
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11-APR-1997;
11-APR-1997;
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97US-0043315P.
97US-0043568P.
97US-0043569P.
97US-0043576P.
                   97US-0043578P
97US-0043580P
97US-0043659P
97US-0043670P
97US-0043671P
97US-0043674P
97US-0043674P
97US-0047501P
97US-0047501P
97US-0047501P
97US-0047581P
97US-0047581P
97US-0047581P
97US-0047582P
97US-0047588P
97US-0047588P
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97US-0040334P.
97US-0040336P.
97US-0040626P.
97US-0043311P.
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97US-0040162P.
97US-0040163P.
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97US-0043314P.
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S-0043311P.
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        22-AUG-1997
23-AUG-1997
23-AUG-1997
25-SEP-1997
05-SEP-1997
05-SEP-1997
05-SEP-1997
05-SEP-1997
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13-JUN-1997;
08-JUL-1997;
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18-AUG-1997;
22-AUG-1997;
    (RUBE/)
(ROSE/)
(SOPP/)
(CART/)
(BEDN/)
(ENDR/)
    NUBEN S M.
ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
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97US-0048974P-
97US-0048974P-
97US-0048974P-
97US-005631P-
97US-0056631P-
97US-005663P-
97US-0056663P-
97US-0056664P-
97US-0056864P-
97US-0056864P-
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97US-005687P-
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97US-005687P-
97US-005687P-
97US-005688P-
97US-00568BP-
97US-005688P-
97US-005688P-
97US-00568BP-
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97US-0047596P.
97US-0047597P.
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97US-0047592P.
97US-0047593P.
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97US-0061660P.
98WO-US004493.
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97US-0057669P.
97US-0057761P.
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97US-0047633P.
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97US-0047613P.
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97US-0047599P.
97US-0047600P.
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97US-0056911P
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The present invention relates to the isolation of novel human secreted CC proteins and the polynucleotide sequences encoding them. The invention CC also discloses vectors, host cells, antibodies, and recombinant methods CC for producing human secreted proteins. The polypeptide and polynucleotide CC sequences for the secreted proteins are useful for preventing, treating, CC ameliorating or diagnosing medical conditions such as hyperproliferative CC disorders (e.g. leukaemia or breast cancers), wounds, reproductive CC thrombocytopaenia), immunodeficiencies (e.g. wiskott-Aldrich syndrome or CC thrombocytopaenia) autoimmune disorders (e.g. wiskott-Aldrich syndrome or CC miltiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma), CC viral or bacterial or fungal infections (e.g. AlDS or sepsis), renal CC disorders (e.g. kidney failure), cardiovascultar disorders (e.g. angina pectoris, cerebral ischaemia or congenital heart defects), respiratory CC disorders, neurological disorders (e.g. Alzheimer's disease or CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The CC Mote: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from the CC USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                 Query Match
Best Local S
Matches 73
                                                                                                                                                                                                Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral ischemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endress (Duan DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 29; 260pp; English.
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(MOOR/)
(SHIY/)
(LAFL/)
(LIYY/)
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(FLOR/)
(OLSE/)
(FISC/)
(EBNE/)
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(FERR/)
(DUAN/)
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(FENG/)
(YOUN/)
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185 GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
187 LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                    39
                                                                                                                1 MVRILANGEIVQDDDFRVRTTTQFFRGSIFRQSFFNRGHGAFFGGFGFRQQQAGARIGAA 60
                                                                                                                                                 Similarity 73; Conserv
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KYAW H.
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FISCHER C L.
EBNER R.
BREWER L A.
MOORE P N.
SHI Y.
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GREENE J M.
FERRIE A M.
DUAN D R.
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LI Y.
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NI J.
FENG F
                                                                            OSPENDLNROLVN 73
                                                    QSPFNDLNRQLVN 111
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                                                                                                                                                  Conservative
                                                                                                                                                61.2%; Score 387; DB 6; 1
100.0%; Pred. No. 9.5e-35;
tive 0; Mismatches 0;
                                                                                                                                                                       Length 111;
                                                                                                                                                  Indels
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  23 MAY 1997
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97US-0047593P
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08-UIL-1997;
16-WIL-1997;
18-AUG-1997;
22-AUG-1997;
23-AUG-1997;
24-AUG-1997;
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23-MAY-1997;
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06-JUN-1997;
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97US-0051926P.
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(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Ro Bednarik DP, Ferrie AM, I , Duan R Shi Y, Rosen CA, P, Endress n R, Hu o, Y, Lafleur DW, GA, Hu J, Fischer CL, Soppet DR GA, Yu G, Ni J, Fer Hu J, Florence KA, Ol Eleur DW, Li Y, Zeng et DR, Ca Feng P, , Olsen F 2 Carter KC;
o, Young PE,
uS, Ebner R,
aw H; Greene

WPI; 1998-506364/43.

New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.

Claim 1; Page 567; 721pp; English.

This sequence represents a secreted human protein encoded by the nucleic acid molecule designated Gene 48 from the human cDNA clone HFCA174 (deposited as clone ATCC 97899 and ATCC 209045). The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511- V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; parkinson's disease; Alzhaimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
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12-SEP-2002 WO200270539-A2

05-MAR-2001; 2001US-00799451. 05-MAR-2002; 2002WO-US005095.

(HYSE-) HYSEQ INC

Tang Wehrman T, Yang Y, T, Wang Zhou P, Yang Y, Ma Goodrich RW, Asundi V, Zh Ma Y, Yamazaki V, Chen R, , Wang D, Drmanac RT; Zhang J, R, Wang i Ŋ Zhao QA, , Ghosh Z

2002-759812/82. DB; ABZ11212.

New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p coagulation disorders. platelet

Claim 9; SEQ ID NO 1042; 1012pp + Sequence Listing; English

The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson or Alzheimer's disease), autoimmune diseases (multiple sclerosis, (Parkinson's weight

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1 Similarity 100.0%; Pred. No. 1.7e-19;
48; Conservative 0; Mismatches 0;
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97US-0040333P

97US-0040334P

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97US-0058P.
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(HUMA-) HUMAN GENOME SCI

Ruben SM, Ro Bednarik DR, Ferrie AM, Rosen CA, Fischer CL, Soppet DP, Carter KC; RR, Endress GA, Yu G, Ni J, Feng P, Young PE, Ouan R, Hu J, Florence KA, Olsen HS, Ebner R, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H; Greene JM; Brewer LA;

2002-634796/68. DB; ABS73545.

preservative. New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or

Example 1; SEQ ID NO 367; 129pp; English.

autonominate diseases e.g. rheumatoid arthritis, hyperproliferative consorders e.g. neoplasms of the breast or liver, cardiovascular disorders c.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, c.g. angiogenesis, nervous system disorders e.g. Alzheimer's disease, c.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents one of the novel human secreted proteins of the invention. Note: This sequence did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6420526B1 The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 c sequences also given in the specification. The protein is used in a pharmaceutical composition used to prevent, treat or ameliorate a medicondition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include a medical CDNA

á 밁 Query Match Best Local S Matches 48 Sequence 48 74 MGFPQWHLGNHAVEPVTSILLLFLLMMLGVRGLLLVGLVYLVSHLSQR 121 48; Н Similarity MGFPQWHLGNHAVEPVTSILLLFLLMMLGVRGLLLVGLVYLVSHLSQR 48 38.8%; ilarity 100.0%; Conservative A, .0%; 0; k; Score 245; DB k; Pred. No. 1.7 0; Mismatches 1.7e-19; 멾 5 0 Length 48 0 Gaps 0

22-SEP-2003 ABO34421 standard; protein; (first entry) 48

of f human secreted protein encoded by cDNA sequence #48.

ABO34421
ID ABO34421
AC ABO34
XX ABO34 Human; secreted protein; hyperproliferative disorder; leukaemia; breast cancer; wound; reproductive disorder; blood-related disorder; haemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia; Miskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis; graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma; viral infection; bacterial infection; fungal infection, AIDS; sepsis; renal disorder; kidney failure; cardiovascular disorder; cytostatic; angina pectoris; cerebral ischaemia; congenital heart defect; respiratory disorder; neurological disorder; Alzheimer's disease; parkinson's disease; inflammation; Crohn's disease; vulnerary; immunosuppressive; antibacterial; haemostatic; thrombolytic; anticoagulant; neuroprotective; thyromimetic; antiallergic;

11-APR-1997
11-APR-1997
11-APR-1997
23-MAY 1997
23-MAY 1997 11-APR-1997; 11-APR-1997; 07-MAR-1997; 16-MAR-2001; 2001US-00809391 97US-0043669P 97US-0043671P 97US-0043672P 97US-0047502P 97US-0047502P 97US-0047503P 97US-0047583P 97US-0047583P 97US-0047588P 97US-0047588P 97US-0047588P 97US-0047588P 97US-0047588P 97US-0047588P 97US-0047598P 97US-0047592P 97US-0047592P 97US-0047592P 97US-0047594P 97US-0047594P 97US-0047591P 97US-0047532P 97US-0047612P 97US-0047613P 97US-0047613P 97US-0047613P 97US-0047632P 97US-0048974P 97US-0048974P 97US-0048974P 97US-0048974P 97US-0048974P 97US-0048974P 97US-0048974P 97US-0043578P. 97US-0043580P. 97US-0040163P

antiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal; cerebroprotective; cardiant; nootropic; antiparkinsonian; antiinflammatory.

sapiens.

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22-AUG-1997
23-AUG-1997
23-AUG-1997
25-SEP-1997
05-SEP-1997
05-SEP-1997
05-SEP-1997
05-SEP-1997
05-SEP-1997
05-SEP-1997
05-SEP-1997
05-SEP-1997
05-SEP-1997
06-SEP-1997
Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA Moore PA Shi Y Lafleur DW Li Y Zeng Z KYaw H;
                                                                                                                                          (ROBE/
(ROSE/)
(SOPP/)
(SOPP/)
(SOPP/)
(ENDR/)
(ENDR/)
(ENDR/)
(FING/)
(FERR/)
(FERR/)
(FERR/)
(FLOR/)
                                                                                                                                    LAFLEUR D W.
LI Y.
ZENG Z.
KYAW H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RUBEN S M.
ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
YU G.
YU G.
FENG P.
FENG P.
GREENE J M.
FERRIE A M.
DUAN D R.
HU J.
HU J.
HU J.
HU J.
                                                                                                                                                                                                                                                                     FLORENCE K A.
OLSEN H S'.
FISCHER C L.
EBNER R.
BREWER L A.
MOORE P A.
SHI Y.
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97US-0056662P

97US-0056664P

97US-0056864P

97US-0056864P

97US-0056875P

97US-0056875P

97US-0056879P

97US-0056879P

97US-0056881P

97US-0056881P

97US-0056888P

97US-0056888P

97US-0056888P

97US-0056888P

97US-0056888P

97US-0056889P

97US-0056889P

97US-0056891P

97US-0056911P

97US-0056911P

97US-005765P

97US-0058765P

97US-0058785P

97US-0058785P
RESULT 11
ABG00633
ID ABG00
XX ABG00
XX Novel
XX Novel
XX Humar
XX Homo
XX Hom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the isolation of novel human secreted proteins and the polynucleotide sequences encoding them. The invention CC proteins and the polynucleotide sequences encoding them. The invention CC also discloses vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The polypeptide and polynucleotide sequences for the secreted proteins are useful for preventing, treating, ameliorating or diagnosing medical conditions such as hyperproliferative disorders (e.g. leukaemia or breast cancers), wounds, reproductive conditions for preventing, treating, and thrombocytopaenia, antoimmune disorders (e.g. wiskott-Aldrich syndrome or continue thypoplassia), antoimmune disorders (e.g. wiskott-Aldrich syndrome or cultiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma), continue of bacterial or fungal infections (e.g. ALDS or sepsis), renal continues (e.g. kidney failure), cardiovascular disorders (e.g. anginae contents), and inflammations (e.g. Crohn's disease). The colymucleotide or polypeptide may also be used as vaccine adjuvants. CC ABO34374-ABO34815 represent human secreted proteins or their fragments. CC Exching the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPPO web site at segdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.8%; Score 245; DB 6; Best Local Similarity 100.0%; Pred. No. 1.7e-19; Matches 48; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral ischemia.
WPI; 2001-639362/73
                                                                                                                                                                            31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                            11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                         WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-2002 (first entry)
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                                                                                                                   (HYSE-) HYSEQ
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DB; ACD82688.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic protein
                                                  Liu C,
                                                                                                                   INC
                                                  Tang
                                                      TY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #624.
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Claim New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

20; SEQ ID NO 30992; 103pp; English.

The invention relates to isolated polymucleotide (I) and polypeptide (II) consequences, (I) is useful as hybridisation probes, polymerase chain creaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes, (I) is useful in gene therapy techniques to restore normal cartivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a CC useful for generating antibodies against it, detecting or quantitating a CC useful for generating antibodies against it, detecting or quantitating a CC of sites expressing (II). (I) and (II) are useful for treating disorders involving abarrant protein expression or biological activity. The CC polypeptide and polymucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in CC electronic format directly from WIPO at CC patentic format format format for this contents format format ftp.wipo.int/pub/published_pct_sequences

Sequence 114 AA;

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101
                    113
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                                                                                                              1 MVRILANGEIVQDDDPRVRTTTQPPRGSIPRQSFFNRGHGAPPGGPGPRQQQAGAR-LGA
                                                                                                                                       56; Conservative
                                                                                                                                                  Similarity
                    ATASHT 118
                                           MVRILANGEIVQDRRP-----PSEDHYP-----ATKRGSVAPASKQARCQGWVL
                                                                 AQSPENDLNRQL-VNMGPPQWHLGNHAVEPV----TSILLFLLMMLGVRGLLLVGLV 112
YLVSHL 106
                                                                                                                                                 29.1%;
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                                                                                                                                      Score 184; DB 4; Length 114; Pred. No. 2.6e-12; 4; Mismatches 3B; Indels
                                                                                        44
                                                                                                               59
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ABB84669 standard; protein; 132

(first entry)

Human SECP-21 protein from clone 1265837CD1 SEQ ID 21

ABSULT 12
ABB4669
ID ABB4467
XX ABB44
AC ABB44
XX 11-FE
XX 11-FE
XX 11-FE
XX Human
XX Secre
KW Secre
KW Antia
KW antia
KW antia
KW vasott
KW vasott
KW antig
KW altog
KW Huntij
KW Gevel hepatotropic; cytostatic; anti-HIV; antiallergic; antiasthmatic; cancer; antianaemic; antidabetic; antiinflammatory; neuroprotective; antiulcer; antirheumatic; antiarthritic; cardiant; hypotensive; gonadal dysgenesis; vasotropic; anticonvulsant; nootropic; immunosuppressive; pericarditis; antiparkinsonian; ophthalmological; cell proliferative disorder; anticonvulsant; alteroscis; cirrhosis; hepatitis; angina pectoris; autoimmune disorder; AIDS; Crohn's disease; multiple sclerosis; epilepsy; ulcerative colitis; cardiovascular disorder; myocardial infarction; Raynaud's disease; myocarditis; neurological disorder; cataract; funtington's disease; myocarditis; neurological disorder; cataract; funtington's disease; Alabelmer's disease; Creutzfeldt-Jakob disease; developmental disorder; Duchenne muscular dystrophy; antipsoriatic; Becker muscular dystrophy; Cushing's syndrome. protein; SECP; human; antiarteriosclerotic; antiatherosclerotic;

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30-MAR-2001; 2001US-0280527P.
06-APR-2001; 2001US-0282111P.
09-APR-2001; 2001US-0282702P.
13-APR-2001; 2001US-0283855P.
19-CCT-2001; 2001US-034371BP.
07-DEC-2001; 2001US-034371BP.
13-FEB-2002; 2002US-0357002P.
                                                                                                                                                                                                                29-MAR-2002; 2002WO-US009820
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                                                                                                                                                                          (INCY-) INCYTE
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Lal ru, Swarnakar A, Ramus... RA. Yao MG, MR, Burford N, Diny AR, Gietzen KJ, Griff, Lu, Lee EA, Lee S, Lu, Far A, Ramkumar J, T, W2, Xu Y, A A , Ding L, Duggan BM, Elli J, Griffin JA, He A, Honc S, Lu DAM, Mason PM, San r J, Tang YT, Thangavelu K Xu Y, Yue H; Elliott VS, Forsythe IJ; Honchell CD, Ison CH; Sanjanwala MM; Plu K, Tran UK, Walia NK;

Novel human secreted protein useful for treating, preventing or diagnosing cancer, hepatitis, psoriasis, asthma, diabetes mellitus, anemia, epilepsy, cataract, Alzheimer's disease.

Claim 76; Page 167; 188pp; English.

CC -HIV, antiallergic, antiastematic, antianemic, antidiabetic, antiinflammatory, neuroprotective, antiuncer, antipsoriatic, vasotropic, continuation, neuroprotective, antiuncer, antipsoriatic, vasotropic, continuation, neuroprotective, antiuncer, antipsoriatic, vasotropic, continuation, antiarthritic, cardiant, hypotensive, anticonvulsant, convoltant, This invention describes novel secreted proteins (SECP) which have antiarteriosclerotic, antiatherosclerotic, hepatotropic, cytostatic-HIV, antiallergic, antiasthmatic, antianaemic, antidiabetic, cytostatic,

Sequence Ą

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                                                                               Query Match
Best Local s
Matches 30
                                    42
                                                                                l Similarity 30; Conserv
GNHAVEPVTSILLLFLLMMLGVRGLLLVGLVYLV 115
                                RGQRPKESEQDVEDSQNHTGEPVGDDYK-----KMGTL---FGELNKNLINMGFTRMYF
                                                         RGSIPRQS----FFNRGHGAPPGGPGPRQQQAGARLGAAQSPFNDLNRQLVNMGFPQWHL 81
                                                                                Conservative
                                                                                         17.5%;
                                                                               Score 110.5;
Pred. No. 0.00
17; Mismatches
                                                                              DB 6;
00042;
les 34;
                                                                                13;
                                                                              Gaps
                                    92
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Length

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93

GERIVEPVIVIFFWVMLWFLGLQALGLVAVLCLV 126

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RESULT 13

RESULT 13

ADERO8064

ID ADERO
XX ADERO
XX ADERO
XX ADERO
XX ADERO
XX NOVE

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Best Local S
Matches 30
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11-DEC-2001; 2001US-0339453P.
14-MAR-2002; 2002US-0365091P.
14-MAR-2002; 2002US-0365384P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-0372558.
22-APR-2002; 2002US-0376045P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein of the invention.
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N-PSDB; ADE07153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 1130; 1177pp; English.
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 132 AA;
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93
                                                            82
                                                                                                                         42
                                                                                                                                                                                     26
                                                                                                                                                                                                                                                  l Similarity
30; Conser
                                                                                                                                                                               RGSIPROS----FFNRGHGAPPGGPGPRQQQAGARLGAAQSPFNDLNRQLVNMGFPQWHL
GERIVEPVIVÍFFWVMLWFLGLQALGLVAVLCLV 126
                                                         GNHAVEBALSITTTETTWWTGARGTTTAGTAXTA 112
                                                                                                                         RGQRPKESEQDVEDSQNHTGEPVGDDYK-----KMGTL---FGELNKNLINMGFTRMYF
                                                                                                                                                                                                                                                  17.5%; Score 110.5; DB 7; larity 31.9%; Pred. No. 0.00042; Conservative 17; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                  Length 132;
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                                                                                                                                                                                                                                                         13;
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                                                                                                                                                                                                                                                         Gaps
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RESULT 15
AAB42404
ID AAB42
XX

AAB42404 standard; protein; 325

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AAG77595

AAG77595

ID AAG77

XX AAG7

XX AAG7

XX Huma

XX Huma

XX Huma

XX Homc

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                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 9643-9644; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer antigen protein SEQ ID NO:8361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG77595 standard; protein; 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-235357/24.
)B; AAH37002.
                                                           67
                                                                                                                                                                                         15 DPRVR-----TTTQPPRGSIPRQSFFNRGHGAPPGGPGPRQQQAGARLGAAQSPFND
   67
                                                                                                                             15
                                                              LNRQLVNMGFPQWHLGNHAVEPVT 90
                                                                                                                             DPRVRPRSSSGSPLVTRVPRAS-PAPEGPASGHGALPGGAGLR---AGHERGAAAR----
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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99US-0163280P.
PRAHGGRSAARPGT 80
                                                                                                                                                                                                                                                                                           12.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4277 human colon cancer-associated polypeptides, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer antigen; diagnosis;
                                                                                                                                                                                                                                                               Score 80; DB 4;
Pred. No. 0.64;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection;
                                                                                                                                                                                                                                                                                                                                     92
                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                        99
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Human ORFX ORF2168 polypeptide sequence SEQ ID NO:4336.

08-FEB-2001

(first entry)

AAB42404;

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CC which represent the human ORFX open reading frames 1 to 3161. The ORFX CC sequences have activitles such as: cytostatic; hepatotropic; vulnerary; CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; ostepathic; CC cardiant; thrombolytic; coagulant; vasctropic; antidiabetic; hypotensive; CC dermatological; immunosuppressive; antiinflammatory; antibacterial; CC antiviral; antifungal; antirheumatic; antiinflammatory; and antianaemic. The csquences can be used for determining the presence of or predisposition conditions associated with an CC ORFX-associated disorder. The nucleic acids can be used to express ORFX CC proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative cdisorders, osteoarthritis, graft vs host disease, cardiovasqular disease, storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune contained damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antiviral; entibacterial; antifungal; antirheumatic; antithyroid; antiviral; gene therapy; cancer; proliferative disorder; hypotension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1999; 99US-0127607P.
05-ARR-1999; 99US-0127636P.
05-APR-1999; 99US-0127728P.
30-MAR-2000; 2000US-00540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-602362/57.
N-PSDB; AAC76613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotectiv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 3531-3532; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000WO-US008621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-2000.
                                                                                        Sequence 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200058473-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
      Conservative
                                                                                        A,
      12.7%; Score 80; DB 3; Length 325; 35.5%; Pred. No. 2.8; tive 13; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nootropic; neuroprotective;
  30;
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        6
    Gaps
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               106 LLLVGLVYLVSHLSQR 121
 84
                                                                          48
                                                   28
LLTFGYLVLLSHVGER 99
                                                   PPQLALGAALVNVQIPL--LLGQLVEVVAKYTRDHVGSFMTE--SQNLSTHLLILYGVQG 83
                                                                         PROQQAGARIGAAOSPENDINROLVNM--GEPOWHIGNHAVEPVISILLIFLLMMIGVRG 105
```

Search completed: August 24, 2004, 09:18:12 Job time : 61 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2004, 09:17:05; Search time 15 Seconds (without alignments) 775.945 Million cell updates/sec

Title: Perfect score: Sequence: US-10-001-885-125
632
1 MVRILANGEIVQDDDPRVRT......GVRGLLLVGLVYLVSHLSQR 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Database :

		4: 5: 1:0	Dir4: *			
Presson and	is reg	No. is the greater the derived b	the number of than or equal d by analysis	r of equa ysis	results to the of the t	predicted by chance to have a score of the result being printed, total score distribution.
					SUMMARIES	IES
Result No.	Score	% Query Match	Length	BG	Ħ	escription
1	83.5	13.2	219	o i	T46472	hypothetical prote
2	8	12.8	7	N	739	idine
w	77.5		692	N	T21095	_
4		12.1	1201	N	A83007	' Р
5	76	12.0	159	N	JQ0145	1 17.3
6	74.5	11.8	1151	N	T18297	inger
o ~	3 2	11.6	200) ⊢	TAVLWC	atora tational moto
w (73		841	N I	T01046	hypothetical prote
10	72.5	•	195	- -	SAVLL1	
11	72.5	11.5	207	N	JQ2167	ō
12	72.5	11.5	433	N	T36122	probable integral
13	72	11.4	214	. ب	SAVLDV	
1 ₁ 2	71.5	11.3	552	۰ ۲	OKERUT.	aspartate chemorec
1 15	71.5	1 L	200) N	AC0/46	Attacopt -
17	71	11.2	345	N	A53138	gas1 homolog - hum
18	71	11.2	618	N	T42664	hetical
19	70.5	•	197	N	S22381	, г
20	70		146	N	E70557	•
21	70	11.1	398	N	T34947	cal
22	70	11.1	2559	N	T09144	nıne
23	9	11.0	231	N	875387	ical prot
24	9	11.0	269	N	T42919	protein tio - atel
25	69.5	11.0	447	N	T50705	gamma-aminobutyrat
26	۰.	11.0	530	N	F87590	ne prot
27		•	214	μ.	SAVLDN	delta large antige
28	69	10.9	255	N	B87595	transcription regu
29	69	10.9	283	, N	GUTASA	insulin promoter i
				,		

Query Match

12.8%; Score 81; DB 2; Length 475;

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
67	67	67	67.5	67.5	68	68.5	68.5	68.5	68.5	68.5	68.5	69	69	69	69
10.6	10.6	10.6	10.7	10.7	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.9	10.9	10.9	10.9
1121	914	260	1747	525	530	653	454	206	195	195	148	1454	495	493	484
N	N	N	N	N	N	N	,	N	N	ь	N	N	N	N	N
A82809	T25220	S22373	A54121	T44445	T48627	T34356	C45340	T37094	853112	SAVLDM	S74589	E84535	G71019	F75113	AG2097
exodeoxyribonuclea	hypothetical prote	proline-rich prote	collagen alpha-4 c	chitinase (EC 3.2.	hypothetical prote	hypothetical prote	nucleocapsid prote	hypothetical prote	delta antigen - he	delta large antige	hypothetical prote	probable retroelem	hypothetical prote	NADH dehydrogenase	serine/threonine k

ALIGNMENTS

RESULT 2 A87396 sensor histidine kinase [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: A87396 R;Mierman, W.C.; Peldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647 A;Accession: A87396 A;Astatus: preliminary A;Molecule type: DNA A;Residues: 1-475 <85TO> A;Cross-references: GB:AE005673; NID:g13422503; PIDN:AAK23165.1; GSPDB:GN00148 C;Genetics: A;Gene: CC1181	Query Match Best Local Similarity 36.5%; Pred. No. 0.56; Matches 23; Conservative 11; Mismatches 24; Indels 5; Gaps 2 A1 APPGGPGPROQOAGARLGAAQSPFNDLNRQLVNMGFPQMHLGNHAVEPVTSILLLFLLMM 100 A1 APPGGAGSVRTRRG-RLGALELPCRPGTSVGFPGEVWGGSSVRPELQVLVLFLVVR 63 Db APPRGAGSVRTRRG-RLGALELPCRPGTSVGFPGEVWGGSSVRPELQVLVLFLVVR 63	RESULT 1 T46472 hypothetical protein DKFZp434N2030.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 C;Accession: T46472 R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000 A;Reference number: Z33034 A;Accession: T46472 A;Accession: T46472 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-219 <aaaa> A;Coss-references: EMBL:AL137488 A;Cross-references: EMBL:AL137488</aaaa>
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25;

Gaps

168

75

204

Misra, T Pg

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hypothetical protein PA5114 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: A83007 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hicke adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbi , Lory, S.; Olson, M.V. Rature 406, 959-964, 2000 Rature 406, 959-964, 2000 A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: A83007
                                                   A;Molecule type: DNA
A;Residues: 1-1201 <STO>
A;Residues: 1-1201 <STO>
A;Cross-references: GB:AE004924; GB:AE004091; NID:g9951407; PIDN:AAG08499.1;
A;Cross-references: Strain PAOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: X
A;Introns: 111/1; 215/2; 469/3; 552/3
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
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A;Reference number: Z19373
A;Accession: T21095
A;Status: preliminary; translated from GB/EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F18H3.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Coles, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                          Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: T21095
Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: CESP:F18H3.3a
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-692 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 EIVQDDDPRV---RTTTQPPRGSIP-----RQSFFNRGHGAPPGGPGPRQQQA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDDDPRVRTTT-QPPRGSIPRQSFFNRGHGAP-PGGPG-----PRQQQAGARLGAAQSP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FYQGPPRQQQ----PQQHSQQPAQQPGQ-----QGQGQSGIVIHGQETLTSHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F-NDLNRQLVNMGFPQWHLGNHAVEPVTSILLLFLLMMLGVRGLLLVGLVYLVSHL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPLIFGDFKVGVRQSD----GRWLVVEPKPTLRFDSWQ------QRILLILLSVIA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQGRPPMRTNDGRPQYGMAPRPA-----GAPRVGGPGVQMGGAPIRQQGPAPRGAPQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTPL 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GARLGAAQSPFNDLNRQLV-----NMGFPQWHLGNHAVEPVTSILLLFLLMMLG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELQIDNGPRFFVRRTPVTPPRPDAPPAGANGRPGAREFFAREG-GAPGGGDNARSAQARD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.0%;
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Pred. No. 7;
9; Mismatches
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UI
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B
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
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                                                                                                                                                                                                                                                                            P., Hickey,
A., Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                GSPDB:GN00:
                                                                                                                                                                                                                                                                               M.J.; Bz
K.; Lim,
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                                                                                              B
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                                                                                                                                                                                                                                                                                                                                                                             R;Tevosian, S.G.; Deconinck, A.E.; Cantor, A.B.; Rieff, H.I.; Fujiwara, Y.; Corfas, G.; Proc. Natl. Acad. Sci. U.S.A. 96, 950-955, 193.
A;Title: FOG-2: A novel GATA-family cofactor related to multitype zinc-finger proteins | A;Reference number: Z18866; MUID:99128343; PMID:9927674
A;Accession: T18297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    zinc-finger protein FOG-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18297
               밁
                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AF107306; NID:g4206772; PID:g4206773; PIDN:AAD12182.1
C;Genetics:
A;Gene: Fog-2
                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-1151 <TEV>
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A; Residues: 1-159 < K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kato, J.; Chu, L.; Kitano, K.; DeVault, J.D.; Kimbara, K.; Chakrabarty, A.M.; Misra, Gene 84, 31-38, 1989
A;Title: Nuclectide sequence of a regulatory region controlling alginate synthesis in A;Reference number: JQ0132; MUID:90108714; PMID:2514124
A;Accession: JQ0145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical 17.3K protein - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Jun-1996
C;Accession: JQ0145
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                                                                                              1042 VIVNGGLKQDERP----TANPQQENISQNTQHEDGHKSPSWISENPLAANENVSPGIPCA 1097
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                                                                                                                                   4 ILANGEIVODDDPRVRTTTQPPRGSIPRQSFFNRGHGAP-----
                                                                                                                                                                            l Similarity
27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
            EEQUSSIAKGVNGASQAPSSGKYCRLCDIQFNNLSNFITHKKF---YCSSHAAEHV 1150
                                                       RQQQAGARL---GAAQSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -159 <KAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAGVPARS-RRRGHGRPPGMVADRSAGPTAGLPAQPRLHDAGASLPGSDPP--
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                                                                                                                                                                              Conservative
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                                                                                                                                                                         11.8%; Score 74.5; I
23.3%; Pred. No. 23;
tive 19; Mismatches
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Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                              from GB/EMBL/DDBJ
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                                                     -- FNDLNRQLVNMGFPQWHLGNHAVEPV
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                                                                                                                                                                                                                  Length 1151;
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                                                                                                                                                                              Indels
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Gaps

72

82

37;

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-PGGPGP Gaps

48

89

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hypothetical protein T16K5.190 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46050
R;Rleger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.;
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23015
A;Accession: T46050
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N;Alternate names: HDag

C;Species: hepatitis delta virus

C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 01-Aug-1997

C;Accession: A30054

R;Kuo, M.Y.P.; Goldberg, J.; Coates, L.; Mason, W.; Gerin, J.; Taylor, J.

J. Virol. 62, 1855-1861, 1988

A;Title: Molecular cloning of hepatitis delta virus RNA from an infected wow A;Reference number; A30054

A;Accession: A30054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
hypothetical protein YUP8H12R.29 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 22-Oct-1999 C;Accession: T01046 R;Theologis, A.; Vysotskaia, V.S.; Osborne, B.I.; Schwartz, J.R.; Federspie:
                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 3
A;Introns: 52/1; 83/1; 153/2; 209/1; 257/3; 278/3; 309/3; 363/3; 424/1; 479/1; 501/1;
A;Note: T16K5.190
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                                                                                                                                                                               문
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Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comment: This virus is a replication-defective hepatitis B virus. Superfamily: hepatitis delta virus large antigen
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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2-205/Product: delta large antigen #status predicted <MAT>
                                                                                                                                                                                 592
                                                                                                                                                                                                                                                        532 DPQHPVSAPPPQGYPPKEGYPPAGYPPPAGYPPPQYPQAGYPPAGYPPPQQGYGQGYPAQ 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 LTEEDERRERRVAGPPVGGV--NPLEGGSRGAPGGGFVPNLQ-----GVPESPFSRTGE 184
                                                                                                                                                                                                                  75
                                                                                                                                                                                                                                                                                             15 DPRVRTTTQPPRGSIPRQSFFNRGHGAPPGGPGPRQQQAGARLGAAQSPFNDLNRQLVNM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 QL---VNMGFPQWHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
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                                                                                                                                                                                                                      GFP 77
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ilarity 27.0%;
Conservative 1
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30.7%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                        Score 73; DB 2;
Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                         Length 651
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      J.R.; Federspiel,
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          N.A.;
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            Kwan
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delta large antigen - hepatitis delta virus (strain CAR)
N;Alternate names: HDAg
C;Species: hepatitis delta virus
C;Species: hepatitis delta virus
C;Apecies: nepatitis delta virus
C;Accession: JQ2167
R;Tang, J.R.; Hantz, O.; Vitvitski, L.; Lamelin, J.P.; Parana, R.; Cova, L.;
J. Gen. Virol. 74, 1827-1835, 1993
A;Ritle: Discovery of a novel point mutation changing the HDAg expression of A;Reference number: JQ2167; MUID:93389437; PMID:8376962
A;Accession: JQ2167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A40247
C;Accession: A40247
R;Lee, C.M.; Bih, F.Y.; Chao, Y.C.; Govindarajan, S.; Lai, M.M.C.
Virology 188, 265-273, 1992
A;Title: Evolution of hepatitis delta virus RNA during chronic infection.
A;Title: Evolution of A40247; MUID:92230225; PMID:1566577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
SAVLL1
                                                                                                                                                                                                            RESULT 11
JQ2167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Comment: This virus is a replication-defective hepatitis C;Superfamily: hepatitis delta virus large antigen C;Keywords: core protein F;2-195/Product: delta large antigen #status predicted <MAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   delta large antigen - h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence.
A;Reference number: Z14227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oefner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A40247; MUID:92230225; A;Accession: A40247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 01-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 1
A; Introns: 74/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: ATSP:YUP8H12R.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB:M84917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: genomic RNA
A; Residues: 1-195 < LEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: hepatitis delta virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: translated from
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Matches
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Best Local S
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                                                                                                                                                                                                                                                                                              183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 IPROSFFNRGHGAPPGGPGPRQ------QAGARLGAAQ-SPFNDLNRQLVNM--GF 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77
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                                                                                                                                                                                                                                                                                              GEGLDARGDRGFP
                                                                                                                                                                                                                                                                                                                                     NRQL---VNMGFP
                                                                                                                                                                                                                                                                                                                                                                            GRITEEDEKRKRRVAGPPTGGVNPLEGGQR--GAPGGGFVPSMQ-----GVPESPFHRH 182
                                                                                                                                                                                                                                                                                                                                                                                                                     GEIVQDDDFRVRTTTQFFRGSIFRQSFFNRGHGAFFGGFGFRQQQAGARLGAAQSFFNDL
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 72.5; Di
Pred. No. 6.1;
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                                                     a hepatitis
                                                                                            Lesbordes,
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delta large antigen - hepatitis delta virus (chimpanzee isolate)

N;Alternate names: HDag

C;Species: hepatitis delta virus

C;Date: 30-Sep-1987 #sequence_revision 31-Dec-1990 #text_change 01-Aug-1997

C;Accession: A26176; A30028

R;Wang, K.S.; Choo, Q.L.; Weiner, A.J.; Ou, J.H.; Najarian, R.C.; Thayer, R.M.; Mullenba

Nature 323, 508-514, 1986

A;Title: Structure, sequence and expression of the hepatitis delta (delta) viral genome.

A;Reference number: A26176; MUID:87014821; PMID:3762705
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A; Residues: 1-207 <TAN>
A; Experimental
A;Cross-references: GB:X04451
A;Note: the mucleotide sequence contains a frameshift error in codon 162 that has been c
R;Wang, K.S.; Choo, Q.L.; Weiner, A.J.; Ou, J.H.; Najarian, R.C.; Thayer, R.M.; Mullenba
Nature 328, 456, 1987
                                                                         A;Accession: A26176
A;Molecule type: genomic RNA
A;Residues: 1-161 <WAN>
A;Cross-references: GB:X0445
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A;Reference number: Z21597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable integral membrane protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text_change
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A;Experimental source: strain A3(2)
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Superfamily: hepatitis delta virus large antigen

Superfamily: hepatitis delta virus large antigen

Keywords: core protein; lipoprotein; methylated carboxyl end; prenylated cysteine

204/Binding site: farmesyl (Cys) (covalent) #status predicted

204/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted
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Best Local :
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 LTEEDERRERRAAGPPVGGV--NPLEGGSRGAPGGGFVPNLQ------GVPESPFSRTGE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 ROLVIMG-----FPOWH 80
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Pred. No. 14;
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A;Gene: tar
C;Superfamily: methyl-accepting chemotaxis protein
C;Superfamily: methyl-accepting chemotaxis protein
C;Keywords: chemotaxis; methylated amino acid; sensory transduction;
F;295,309/Modified site: glutamate methyl ester (Gln) (by cheB-depend
F;302,491,500/Modified site: glutamate methyl ester (Glu) #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Russo, A.F.; Koshland Jr., D.E. Science 220, 1016-1020, 1983
A;Title: Separation of signal transduction and adaptation A;Reference number: A03441; MUID:83197387; PMID:6302843
A;Accession: A03441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 1-245, 'E', 247-552 <MOW>
C; Comment: This protein responds to
arious levels of methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Salmonella typhimurium
C;Species: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 15-Aug-1997
C;Accession: A0341; A29053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: residues 294-296, 301-302, 308-309, 483-484, 490-491, R;Mowbray, S.L.; Foster, D.L.; Koshland Jr., D.E.
J. Biol. Chem. 260, 11711-11718, 1985
A;Title: Proteolytic fragments identified with domains of the A;Reference number: A29053; MUID:86008217; PMID:2995347
A;Accession: A29053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-552 < RUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aspartate chemoreceptor protein - Salmonella typhimurium N.Alternate names: methyl-accepting chemotaxis protein I
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A;Molecule type: genomic
A;Residues: 1-214 <WA2>
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                                                                                                                                                                                                                                                                                  Query Match
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Best Local
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212
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                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
IRHALLNPLARVITHIRE 229
                                                  VRGLLLVGLVYLVSHLSQ 120
                                                                                                        QNALGEALGNYARVSENLYROTFDQSAHDYRFAQWQLG-----VLAVVLVLILMVVWFG
                                                                                                                                                                 QQQAGARLGAAQSPFNDLNRQLVNMG----FPQWHLGNHAVEPVTSILLLF1LMML--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RQL---VNMGFPQWHL 81
                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                 11.3%; Score 71.5;
28.2%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not shown; translation not
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8
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                                                                                                                                                                                                                                                                               Length 552;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          concentration
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RESULT 15

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methyl-accepting chemotaxis protein II [imported] - Salmonella enterica subsp. enterica (;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: ACC746
C;Accession: ACC746
C;Accession: ACC746
C;Accession: ACC746
C;Cancar, P.;Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrax,
S: Moule, S: O'Gaora, P.
A;Authbors: Parry C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: ABO502; MUID:21534947; PMID:11677608
A;Accession: ACC746
A;A
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2004, 09:17:04; Search time 9 Seconds (without alignments) 700.054 Million cell updates/sec

Title:
Perfect score:
Sequence: US-10-001-885-125
632
1 MVRILANGEIVQDDDPRVRT......GVRGLLLVGLVYLVSHLSQR 121

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 141681 seqs, 52070155 residues

141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17 .	16	15	14	13	12	11	10	9	80	7	თ	IJ	4	ω	2		No.	Result
Ġ	65.5		66	66	66	•	9	9	φ.		66.5	67	68	æ	œ	68.5	œ	69	69	69	70	70.5	71	71	71		71.5	72	72	72.5	73		Score	
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AMBN_MOUSE	PMP3_MOUSE	CUT1_HUMAN	HS70_AJECA	TES1_RAT	IPF1_RAT	IF2_PROMM	AB10_HUMAN	DNAK_STRGR	V1AR_RAT	LYOX_CHICK	HXD4 HUMAN	POLG_ECO6C	APB1_RAT	PCH8_HUMAN	NCAP CVMS	AANT_HDVM2	AANT HDVM1	IPF1 MESAU	IPF1_HUMAN	AANT_HDVNA		CBL2_MOUSE	CTF8 HUMAN	GAS1_HUMAN	34KD MYCPA	MCP2_SALTY	FA10_RABIT	AD11_HUMAN	AANT HDVIT	AANT_HDVL1	AANT HDVWO	Ö.	ID	
O55189 mus musculu	mus mu	P39880 homo sapien	Q00043 ajellomyces			Q7v5m4 prochloroco	Q9nrk6 homo sapien	5 stre	rattus	gallı	homo sa	e ge	rattue	O95206 homo sapien	murine	hepatitis	hepatitis	118 me		hе		mus 1	homo	6 homo	mycol	P02941 salmonella	5 oryc	pie	4 hepa	9833 hepat	7 hepatitis	nut2 homo sapie	Description	

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SSB3_HUMAN	PECM ERWCH	CAIA BOVIN	ENV MLVHO	ARAF PIG	SYC_SALTY	SYC SALTI	ITAS_BOVIN	HRCA BRAJA	NCO2_MOUSE
		P23206 bos taurus P21519 drosophila							Q61026 mus musculu

ALIGNMENTS

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3888888888	###### ######	RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	RA RA	R R R R R R C C C C G	RESU ABC8 ID AC DT DT DT DE
Name=Eduly; IsoId=QNUT2-1; Sequence=Displayed; Name=Short; IsoId=QNUT2-2; Sequence=VSP_000026; IsoId=Nounce=Nounce=VSP_000026; IsoId=Number=Nounce=Nounce=VSP_000026; IsoId=Number=Nounce	kamura Y.; twenty-six genetic variations: -binding cassette, subfamily B ation."; 47.38-50(2002). (onomer (Potential). R LOCATION: Integral membrane p. rane. F PRODUCTS: rnative splicing; Named isoform.	Salto K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Kanehoti K.; Masuho Y., Kanehoti K.; "MEDO human cDNA sequencing project."; "NEDO human cDNA sequencing project."; "Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. [3] [3] [4] [7] [8] [8] [8] [9] [9] [9] [9] [9] [9] [9] [9] [9] [9	ig cassette membrane protein."; L. Biol. 285:379-389(1999). NCE FROM N.A. (ISOFORM LONG). SePlacenta; LT., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., LT., Ota T., Hayashi K., Sugiyama T., Fujimori K., LT., Ota T., Nagai K., Sugano S., Ishibashi T., Fujimori K., H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,	Homo sapiens (Human). Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1] [1] SEQUENCE FROM N.A. (ISOFORM SHORT), AND MUTAGENESIS. MEDILNE=99096930; PubMed=9878413; Hogue D.L., Ling V., Ling V.	RESULT 1 ABC8 HUMAN STANDARD; PRT; 735 AA. AC Q9NUT2; 095787; DT 16-OCT-2001 (Rel. 40, Created) DT 16-OCT-2001 (Rel. 40, Last sequence update) DT 28-PEB-2003 (Rel. 41, Last annotation update) DE ATP-binding cassette, sub-family B, member 8, mitochondrial precursor DE (Mitochondrial ATP-binding cassette 1) (M-ABC1).

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DR EMBL; AK002018; BAA92038.1; -.

DR HSSP; P13569; INBD.

DR Genew; HCWC149; ABCB8.

DR GO; GO:0005524; C:membrane fraction; TAS.

DR GO; GO:0005524; F:ATP-binding cassette (ABC) transporter acti. ..; TAS.

DR GO; GO:0005524; F:ATP-binding cassette (ABC) transporter acti. ..; TAS.

DR GO; GO:0005215; F:transport; TAS.

DR GO; GO:0005215; F:transporter activity; TAS.

DR GO; GO:0005215; F:transporter activity; TAS.

DR GO; GO:0005216; F:transporter activity; TAS.

DR GO; GO:0005216; F:transporter activity; TAS.

DR GO; GO:0005216; ABC_TRANSPORTER.

DR InterPro; IPR003439; ABC_TRANSPORTER.

DR PFAm; PF00064; ABC_membrane; 1.

DR PFAm; PF00005; ABC_TMIF; 1.

DR PFAM; DR GO:00121; ABC_TMIF; 1.

DR PROSITE; PS00929; ABC_TRANSPORTER.

DR PROSITE; PS009211; ABC_TRANSPORTER.

DR PROSITE; PS00929; ABC_TRANSPORTER.

DR PROSITE; PS009211; ABC_TRANSPORTER.

DR PROSITE;
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Best Local S
Matches 25
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
TRANSMEM
P29997;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Delta antigen.
Hepatitis delta virus (isolate Woodchuck) (HDV).
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                       157
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4
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                  LVLLSHVGER
                                                                                                                                                                                                                     VYLVSHLSQR 121
: |:||: :|
                                                                                                                                                                                                                                                                      GAALVNVQIPL--LLGQLVKVVAKYTRDHVGSFMTE--SQNLSTHLLLLXGVQGLLTFGY
                                                                                                                                                                                                                                                                                                            GARLGAAQSPFNDLNRQLVNM--GFPQWHLGNHAVEPVTSILLLFLLMMLGVRGLLLVGL
                                                                                                                                                                                                                                                                                                                                                                                                                      735 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       512
174
239
278
326
347
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145
196
296
383
507
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                                                                                                           STANDARD;
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165
216
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                                                                                                                                                                                                                                                                                                                                                              11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                      79947 MW;
                                                                                                                                                                                                                                                                                                                                           ; Score 75; DB:
; Pred. No. 9.9;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VAR 013331.

/FTId=VAR 013331.

GK->AR: RENDERS THE F
K -> B (IN REF. 2).

N -> D (IN REF. 2).

N -> T (IN REF. 2).

H -> Q (IN REF. 2).

L -> F (IN REF. 2).

L -> F (IN REF. 2).

R -> H (IN REF. 2).
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V -> I.
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                                                                                                                                                                                                                                                                                                                                                                                                                      879519858F7EC7A6 CRC64;
                                                                                                           205 AA
                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 735;
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-AANT HDVL1

P29833;

01-APR-1993

01-APR-1993

01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                      Delta antigen.
Hepatitis delta virus (isolate Lebanon-1) (HDV).
Viruses; Deltavirus.
NCBI_TaxID=31763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M21012; AAA45723.1; ALT_TERM.
PIR; A30054; SAVLWC.
InterPro; IPR002506; HDV ag.
Pfam; PF01517; HDV ag; 1.
Probom; PD002887; HDV ag; 1.
Antigen; RNA-binding; Muclear protein; Phosphorylation SEQUENCE 205 AA; 23047 MW; 8B33C773B7872B98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=31764;
                                                                                                                                                                                                                                                                                                                                                                                                                                       133 LTEEDERRERRVAGPPVGGV--NPLEGGSRGAPGGGFVPNLQ-----GVPESPFSRTGE 184
                                                                                                                                                                                                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 IVQDDDPRVRTTTQPPRGSIPRQSFFNRGHGAPPGGPGPRQQQAGARLGAAQSPFNDLNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.6%;
Similarity 30.7%;
                                                                                                                                                                                                                                                                                                                                                                                      GLDIRGNQGFP-WDI 198
                                                                                                                                                                                                                                                                                                                                                                                                             OL---VNWGEFOWHL 81
                                                                                                                                                                                                                                                                        (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 25, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                           STANDARD;
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Best Local (
                                                                                                     RNA-BINDING SPECIFICITY.

RNA-BINDING SPECIFICITY.

Lin J.-H., Chang M.F., Baker S.C., Govindarajan S., Lai M.M.C.,

"Characterization of hepatitis delta antigen: specific binding the hepatitis delta virus RNA.",

J. Virol. 64.4051-4058(1990).

-i- SUBCELLULAR LOCATION: Nuclear.

-i- PTM: Phosphorylated.

-i- DISEASE: BINDS SPECIFICALLY TO ANTISERA FROM PATIENTS WITH (

HEPATITIS DELTA VIRAL INFECTIONS.

-i- MISCELLANEOUS: Delta antigen binds specifically to HDV RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A40247; SAVLLL.
PIR; A40247; SAVLLL.
InterPro; IPR002506; HDV_ag.
Pfam; PF01517; HDV ag; 1.
ProDom; PD002887; HDV ag; 1.
ProDom; PD002887; HDV ag; 1.
ProDom; PD002887; MOZ ag; 1.
Antigen; RNA-binding; Nuclear protein; Phosphorylation.
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[4]
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Wang K.S., Choo Q.L., Wein Thayer R.M., Mullenbach G
Nature 328:456-456(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-JRP-1993 (Rel. 25, Last annotation update)
Delta antigen (Alpha antigen).
Hepatitis delta virus (isolate Italian) (HDV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AANT_HDVIT
                                                                                                                                                                                                                                                                                                                                                           MEDLINE-88230601; PubMed-3373572;
Chang M.F., Baker S.C., Soe L.H., Kamahora T., Keck J.G., Makino
Govindarajan S., Lai M.M.C.;
"Human hepatitis delta antigen is a nuclear phosphoprotein with R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WADDLINE=87014821; PubMed=3762705; Wang K.S., Choo Q.L., Weiner A.J., Ou J.H., Najarian R.C., Wang K.S., Choo Q.L., Weiner A.J., Ou J.H., Najarian R.C., Houghton M.; Thayer R.M., Mullenbach G.T., Denniston K.J., Gerin J.L., Houghton M.; "Structure, sequence and expression of the hepatitis delta (delta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HDVIT
                                                                                                                                                                                                                                                                                                                                              binding activity
                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 323:508-514(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; Deltavirus.
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PIR; A40247; SAVLL1.
InterPro; IPR002506; HDV_ag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                              Virol. 62:2403-2410(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome."
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ch G.T., Denni
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Pred. No. 4.
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Denniston K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                           is a nuclear phosphoprotein with RNA-
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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195;
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Best Local S
Matches 25
                                                                           Katagiri T., Harada Y., Emi M., Nakamura Y.;
"Human metalloprotease/disintegrin-like (MDC
organization and alternative splicing.";
Cytogenet. Cell Genet. 68:39-44(1995).
-!- FUNCTION: Probable ligand for integrin in
-!- SUBCELLULAR LOCATION: Type I membrane pro
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75017 HUMAN STANDARD; PRT; 769 AA.
775073; Q14808; Q14809; Q14810;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
ADAM 11 precursor (A disintegrin and metalloproteinase domain 11)
(Metalloproteinase-like, disintegrin-like, and cysteine-rich proteinase)
                                                                                                                                                                                                                                                                                                                                                                                    Sagane K., Ohya Y., Hasegawa Y., Tanaka I.;
"Metalloproteinase-like, disintegrin-like, cysteine-rich proteins MDC2
and MDC3: novel human cellular disintegrins highly expressed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X04451; CAA28050.1; ALT_SEQ.
PIR; A26176; SAVLDV.
InterPro; IPRO02506; HDV ag.
Pfam; PF01517; HDV ag; 1.
Probom; PD002887; HDV ag; 1.
Antigen; RNA-binding; Nuclear protein; Phosphorylation.
SEQUENCE 214 AA; 24078 MW; 83221B6EED0A2688 CRC64;
                                                                                                                                                                               MEDLINE=95044425; PubMed=7956356;
                                                                                                                                                                                                             SEQUENCE OF 106-769 FROM N.A.
                                                                                                                                                                                                                                                      somatically
                                                                                                                                                                                                                                                                              MEDLINE=94073190; PubMe
Emi M., Katagiri T., Ha
Kasumi F., Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                   "A novel metalloprotease/disintegrin-like
                                                                                                                                                                                                                                                                                                                      rissum=Cerebellum;
                                                                                                                                                                                                                                                                                                                                                              Biochem. J. 334:93-98(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98359734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADAM11 OR MDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM LONG).
     IsoId=075078-1; Sequence=Displayed;
Name=Short; Synonyms=MDC-524;
IsoId=075078-2; Sequence=VSP_005472, VSP_005473, VSP_005474,
                                                    Name=Long; Synonyms=MDC-769
                                                               Event=Alternative splicing;
                                                                                                                                                                                                                                        Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 LTEEDERRERRVAGPPVGGVIPLE---GGSRGAPGGGFVPSLQ-----GVPESPFSRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 IVQDDDPRVRTTTQPPRGS-IPRQSFFNRGHGAPPGGPGPRQQQAGARLGAAQSPFNDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQL---VNMGFPQWHL
                                                                                                                                                                                                                                        rearranged in two primary breast 5:151-157(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                        PubMed=8252040;
T., Harada Y., Saito
                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9693107;
                                                                                                                                                                                                                                                                                                                                      (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 72; DB 1
Pred. No. 5.3;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                      SHORT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                              (ISOFORMS
                                                               Named isoforms=2;
                                                                                                                                                                                                                                                                                           Η.,
                                                                                                                                                          (MDC)
                                                                                                                                                                                                              LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 214;
                                                                                          protein
                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                              Inazawa
                                                                                                                  'n
                                                                                                                                                                                                                AND
                                                                                                                                                                                                                                                      cancers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                    the
                                                                                                                                                          gene:
                                                                                                                                                                                                                                                                   at 17q21.3 is
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                                                                                                                    brain.
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                                                                                                                                                                                                                                                                                           J., Ito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
; Homo.
                                                                                                                                                           exon-intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein)
                                                                                                                     5
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REMBL; D17390; BAA32152.1; -.

REMBL; D17390; BAA06471.1; -.

REMBL; D31872; BAA06670.1; -.

REMBL; D31872; BAA06671.1; -.

REMBL; D31872; P. SAA06671.1; -.

REMBL; D31872; BAA06671.1; -.

REMBL; D31872; P. SAA06671.1; -.

REMBL; D31872; BAA06671.1; -.

REMBL; D31872; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00200; disintegrin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
PRODOM; P0000664; Disintegrin; 1.
PROSOM; SM00608; ACR; 1.
SMART; SM00050; DISIN; 1.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS00427; DISINTEGRIN 1; FALSE_NEG.
PROSITE; PS000427; DISINTEGRIN 2; 1.
PROSITE; PS00022; EGF 1; 1.
PROSITE; PS00022; EGF 1; TALSE_NEG.
PROSITE; PS00026; EGF 2; FALSE_NEG.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
Signal; Glycoprotein; Transmembrane; EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DISEASE: Rearrangements occur in breast and ovarian cancers which involve multiple exons and disrupt the coding region.
-!- SIMILARITY: Belongs to peptidase family M12B.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 disintegrin domain.
PROPER CHAIN
DOMAIN
TRANNEM
DOMAIN
DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Glyo
Alternative
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DISEASE: Rea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSP_005475;
TISSUE SPECIFICITY: Expressed predominantly in brain. Slighly detected or not at all in other tissues.

DOMAIN: A conserved motif [AVN(B/D)CD] within the disintegrin-like domain could be involved in the binding to the integrin receptor.

PTM: The precursor is cleaved by a furin endopeptidase (By eighteen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         splicing
   23
225
769
7534
7098
7098
7098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEASE; FALSE NEG.
Transmembrane; EGF-like
                                                                                                                                                                                                       ADAM 11.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
METALLOPROTEASE-LIKE.
DISINTEGRIN-LIKE.
CYS-RICH.
BGF-LIKE.
BY SIMILARITY.
POTENTIAL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY.
      .) (POTENTIAL).
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RESULT 6
PARABIT
FAIO RABIT
FAIO PARABIT
FAIO PARABIT
FAIO PARABIT
FAIO PARABIT
FAIO CONTROL
DT 15-DEC
DT 
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A Pendurth! U.R., Anderson K.D., James H.L.;

Pendurth! U.R., Anderson K.D., James H.L.;

Thromb. Res. 85:503-514(1997).

Thromb. Res. 85:503-514(1997).

C -!- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, C calcium and phospholipid during blood clotting.

C -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg--Thr and then Arg-|-IIE bonds in prothrombin to form thrombin.

C -!- SUBUNIT: The two chains are formed from a single-chain precursor by the excision of two Arg residues and are held together by 1 or more disulfide bonds.

C -!- FIM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium (By control of the control of the calcium of some glutamate residues allows the modified protein to bind calcium (By control of the calcium of the calcium of some calcium of the calcium of some calcium of the calcium of some c
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Best Local S
Matches 23
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CARBOHYD
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   019045;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FA10_RABIT
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N-LINKED (GLCNAC. . .) (POTENTIAL).

Missing (in isoform Short).

/FTId=VSP_005472.

DLELN -> MCMLS (in isoform Short).

/FTId=VSP_005473.

DVLCGFLLCVNISGAPRLGDLVGDISSVT -> PQQGRAVW
LPPLCQHLWSSSARGPGGRHQ (in isoform Short).

/FTId=VSP_005474.

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/FTId=VSP_005475.
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D -> N (IN REF. 2).
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(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).

Calcium also binds, with stronger affinity to another site, beyond the GLA domain.

SIMILARITY: Belongs to peptidase family \$1.

SIMILARITY: Contains 2 EGF-like domains.

similarity).

PTM: N- and O-glycosylated (By similarity).

PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE EXTRINSIC PATHWAY).

INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)

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PRINTS; PRO0722; CHYMOTRYPSIN.

PRINTS; PRO0010; EGFBLOOD.

PRINTS; PRO0011; GLABLOOD.

SMART; SM000179; EGF_CA; 1.

SMART; SM00029; GLA; 1.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS01186; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS001187; EGF_CA; 1.
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InterPro; IPR000003; C
InterPro; IPR001881; E
InterPro; IPR001881; E
InterPro; IPR001893; E
InterPro; IPR006209; E
InterPro; IPR0062383; G
InterPro; IPR0062383; G
InterPro; IPR001314; P
InterPro; IPR001314; P
InterPro; IPR0002343; G
InterPro; IPR001314; P
InterPro; IPR0002343; G
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Pfam; PF00089; trypsin; 1.
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ACTIVATED FACTOR XA, HEAVY C
EGF-LIKE 1, CALCIUM-BINDING
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McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium

LT2.";
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Russo A.F., Koshland D.E. Jr.;
"Separation of signal transduction and adaptation functions
aspartate receptor in bacterial sensing.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P02941;
21-JUL-1986 (Rel. 01, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Methyl-accepting chemotaxis protein II (MCP-II)
  X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 26-188.
MEDLINE=92073901; PubMed=1660187;
Millburn M.V., Prive G.G., Milligan D.L., Scott W.G., Yeh
Jancarik J., Koshland D.E. Jr., Kim S.H.;
"Three-dimensional structures of the ligand-binding domai
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STRAIN=LT2 / SGSC1412 / ATCC 700720;
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Enterobacteriaceae; Salmonella
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PDB; 1WAT; 15-JAN-95.

PDB; 2LIG; 15-SEP-95.

PDB; 1LIH; 15-SEP-95.

PDB; 1VLS; 21-APR-97.

PDB; 1VLT; 15-MAX-97.

PDB; 1JNW; 22-AUG-01.
                                                     PRINTS; PRO0260; CHEMTRUSDUCR.
SWART; SM00204; HAMP; 1.
SWART; SM00208; WA; 1.
SWART; SM00283; WA; 1.
SWART; SM00319; TarH; 1.
SROSTE; PS0538; CHEMOTAXIS TRANSDUC 1; 1.
PROSITE; PS50111; CHEMOTAXIS TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 1.
Chemotaxis; Transducer; Transdembrane; Methylation; Periplasmic;
               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                  StyGene; SG10387; tar.
InterPro; IPR004091; AspME chemrecept.
InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR00360; HAMP.
InterPro; IPR003099; Me chemotaxis.
InterPro; IPR003122; TarH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                     Pfam; PF00672; HAMP; 1.
Pfam; PF00015; MCPsignal; 1.
Pfam; PF02203; TarH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93252857; PubMed=8486661; Yeh J.I., Blemann H.-P., Pandit J., Koshland D.E., Kim S.-H.; Yeh J.I., Blemann H.-P., Pandit J., Koshland D.E., Kim S.-H.; "The three-dimensional structure of the ligand-binding domain of a wild-type bacterial chemotaxis receptor. Structural comparison to the cross-linked mutant forms and conformational changes upon ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 26-180.
MEDLINE=96428686; PubMed=8831788;
Yeh J.I., Biemann'H.-P., Prive G.G., Pandit J., Koshland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacterial aspartate receptor with and without a ligand.", Science 254:1342-1347(1991).
DOMAIN
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                                               inner membrane; 3D-structure;
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AE008785; AAL20835.1; -.
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             COMPLETE PROTEOME.
CYTOPLASMIC (POTENTIAL).
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 PERIPLASMIC (POTENTIAL)
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               EMBL; X68102; CAA48221.1;
PIR; A40616; A40616.
Antigen; Transmembrane.
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                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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   Transmembrane.
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ilarity 28.2%;
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Pred. No. 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 kDa antigenic protein.

Mycobacterium paratuberculosis.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium.

MCBI_TaxID=1770;
                                                                                                                                                                                                                                                               Gilot P., de Kesel M., Machtelinckx L., Coene M., Cocito C.; "Isolation and sequencing of the gene coding for an antigenic 34-kilodalton protein of Mycobacterium paratuberculosis."; J. Bacteriol. 175:4330-4935(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
30-YAY-2000 (Rel. 39, Last annotation update)

    -!- SUBCELLULAR LOCATION: Integral membrane protein.
    -!- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV0954.

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E -> G (IN REF. 1).
T -> A (IN REF. 1).
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THE 3 ARG MAY FORM A POSITIVELY CHARGED POCKET, WHICH BINDS THE ALPHA-CARBOXYL GROUP OF THE ATTRACTANT AA.
DEAMLIDATION AND METHYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHYLATION.
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§ EMBL outstation -

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NCBI_TaxID
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch);
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01-OCT-1996 (Rel. 34, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Growth-arrest-specific protein 1 precu
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P54826;
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                                                                                                                                                                                                                                                                                                                                 growth-suppressing huma Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                               del Sal G.,
Schneider C.
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94173926; PubMed=8127893;
del Sal G., Collavin L., Ruaro M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAS1.
                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                      "Structure, function, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                    suppression. Blocks entry to S phase. Prevents normal and transformed cells.
                                                                                                                                                                                                                                                                                  similarity).
                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                        FUNCTION: Specific growth
                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a cen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
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Sci. U.S.A. 91:1848-1852(1994).
ific growth arrest protein involved
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Primates;
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                                                                                       regulation of cell proliferation; TAS. regulation of S phase of mitotic c. Signal; Glycoprotein; Lipoprotein.
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Pred. No. 9
                              GROWTH-ARREST-SPECIFIC I
REMOVED IN MATURE FORM (
POLY-ALA.
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POTENTIAL.
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  GPI-anchor amidated serine N-LINKED (GLCNAC. . .) (PO: 2AAD50F1D3632F9D CRC64;
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  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Clagg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clagg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clagg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clagg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
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RA Clagg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clagg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clagg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clagg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hight R.E., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., King A., King A., King A., King A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Rice C.M., Ross M.T., Soott C.E., Sehra H.K., Showhkeen R., Sims S.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Milne S.L., Whittaker P., Willey D.L., Walliams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
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Q96D72; Q9UFB6;
28-FEB-2003 (Re
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11780052;
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Primates;
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Pred. No.
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28-FEB-2003
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CONFLICT
-!- SUBUNIT: Binds to CDK3, CDK5 and c-AB
like region binds to CDK5.
-!- TISSUE SPECIFICITY: Widely expressed.
-!- SIMILARITY: Belongs to the cyclin fam
                                                                                                                                    Biochim. Biophys. Acta 1574:157-163(2002).
                                                                                                                                                                                                                         TISSUE=Liver, and Spleen;
MEDLINE=21952370; PubMed=11955625;
MEDLINE=21952370; PubMed=11955625;
Sato H., Nishimoto I., Matsuoka M.;
"Ik3-2, a relative to ik3-1/cables, is associated with cdk3,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cdk5 and abl enzyme
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AL035669; CAC12754.1; ALT_INIT.
BC012757, AAH12757.1; -.
HGNC:16151; C20orf158.
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253
478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
1 enzyme substrate 2 (Interactor with cdk3 2) (Ik3-2).
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ilarity 35.4%;
Conservative
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253 ·A
53940 MW;
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; Pred. No. 1
4; Mismatch
                                                                             CDKS and c-ABL. The
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A -> P (IN REF. 3).
EECD3CFD70BA3FD0 CRC64;
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                                                                                 C-terminal cyclin-box-
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Best Local S
Matches 23
                                                                                                                                                                                                              GO; GO:0005515; F:protein binding; InterPro; IPR006671; Cyclin_N. Ffam; PF00134; cyclin; 1. Cell cycle; Cell division; Cyclin. Cell cycle; Cell division; Cyclin. DOMAIN 7 11
                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                       EMBL; AY049712; AAL12171.1; -.
                                                                                                                                                                                                                                                                                        MGD; MGI:2182335; Cables2
 318
                                                            269 PRPSIPR-----
                              81 LGNH 84
                                                                                          25
                                                                                                                                      Similarity
CGKH 321
                                                                                    PRGSIPROSFFNRGHGAPPGG----PGP-RQQQAGARLGAAQSPFNDLNRQLVNMGFPQWH
                                                                                                                                                                                  15
481 AA;
                                                                                                                    11.2%;
ilarity 35.9%;
Conservative
                                                                                                                                                                       11 POLY-ALA.
113 PRO-RICH.
52710 MW; 00DA1C706578B1B2 CRC64;
                                                            -APPGSRHKPVPTKSTPAGTELGSDGGDAVEXNPNLLD--DPQWP
                                                                                                                   ; Score 70.5; DE; Pred. No. 17; 5; Mismatches
                                                                                                                                                                                                                                                                             IPI.
                                                                                                                                                  DB 1; Length 481;
                                                                                                                      21;
                                                                                                                        Indels
                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                  collaboration
                                                                                                                      Gaps
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RASULT 12

$24A_ARATH

ID $24A_ARATH

AC Q9SFUO;

DT 16-CCT-2001 (Rel. 40, Last sequence update)

DT 16-CCT-2001 (Rel. 40, Last annotation update)

DT 16-CCT-2001 (Rel. 40, Last annotation update)

DT 16-CCT-2001 (Rel. 40, Last sequence update)

RA Balmoubate update upda
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                                                                                                                                                                                                                                                                                                                                    RESULT 13
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Best Local S
Matches 23
                                                                                                                                                                                                                               01-MAY-1992
01-MAY-1992
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR00123; Gelsoln.
InterPro; IPR006900; Sec23_trunk.
InterPro; IPR006900; Sec23_trunk.
InterPro; IPR006895; zf-Sec23_Sec24.
Pfam; PR00626; Gelsolin; 1.
Pfam; PP04815; Sec23_helical; 1.
Pfam; PP04811; Sec23_trunk; 1.
Pfam; PP04810; zf-Sec23_Sec24; 1.
Pfam; PP04811; Sec23_Sec24; 1.
Pfam; PP04811; Sec23_Sec24; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 408:820-822(2000).

-- FUNCTION: Component of the COPII coat, that covers ER-derived vesicles involved in transport from the endoplasmic reticulum to the Golgi apparatus. COPII is composed of at least five proteins: the SEC33/24 complex, the SEC13/31 complex, and the protein SAR1. Acts in the cytoplasm to promote the transport of secretory, plasma membrane, and vacuolar proteins from the endoplasmic plasma membrane, and vacuolar proteins from the endoplasmic reticulum to the Golgi complex (By similarity).
                                            MEDLINE-91020976; PubMed-2219700; Chao Y.C., Chang M.F., Gust I., Lai M. "Sequence conservation and divergence Virology 178:384-392(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A., Makayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; "Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                 Delta antigen.
Hepatitis delta virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      AANT HDVNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                              NCBI_TaxID=10426;
                                                                                                                                                                                   Viruses; Deltavirus.
                                                                                                                                                                                                                                                                                                                      HDVNA
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              PTM: Phosphorylated.
DISEASE: BINDS SPECIFICALLY TO ANTISERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 PPFPTTQNPPQGPPPPQTL--AGHLSPPMSLRPQQPMAPVAMGPPP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 11.1%;
l Similarity 30.7%;
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     LP----GANAYPPAT 176
                                                                                                                                                                                                                                                                                                                                                                                                                       FPOWHLGNHAVEPVT 90
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(Rel:
(Rel:
                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                   sequence update)
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Pred. No. 44;
6; Mismatches
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                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13FAB74147EAB9C8 CRC64;
                                                                                                                                                                                                                                                                                                        214 AA.
                                                                                                  .M.C.;
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                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                 hepatitis
                   FROM PATIENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                  delta
                                                                                  virus RNA.";
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                   WITH CHRONIC
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RESULT 14
ALD DESCRIPTION OF THE PROPERTY OF THE PROPERT
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Best Local
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TIGSUE=PARCYCRATIC islets;
MEDLINE=96220081; PubMed=8635654;
MEDLINE=96220081; PubMed=8635654;
Inoue H., Riggs A.C., Tanizawa Y., Ueda K., Kuwano A., Liu L.,
Inoue H., Riggs A.C., Tanizawa Y., Ueda K., Kuwano A., Liu L.,
Inoue H., Permutt M.A.;
Paris-Keller H., Permutt M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPP1_HUMAN STANDARD; PRT; 283 AA.

PS2945; 060594;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
11sullin promoter factor-1 (IPF-1) (Pancreas/duodenum homeobox-1) (IDX-1) (Somatostatin transactivating factor-1) (STF-1) (Insulin upstream factor-1) (IUF-1) (Glucosesensitive factor) (GSF).
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   SEQUENCE FROM N.A. TISSUE=Pancreatic islets; Marshak S., Totary H., Cerasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002506; HDV_ag.
Pfam; PF01517; HDV ag; 1.
ProDom; PD002887; HDV_ag; 1.
Antigen; RNA-binding; Nuclear protein; Phosphorylation.
SEQUENCE 214 AA; 24180 MW; 91F2D28B55EC801D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Localization of human homeodomain transcription factor insulin promoter factor 1 (IPF1) to chromosome band 13q12.1."; Genomics 28:125-126(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=96070447; Stoffel M., Stein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- MISCELLANEOUS: Delta antigen binds specifically to HDV RNA.
                                                                                                                           Submitted
                                                                                                                                                                                    ISSUE=Pancreatic
                                                                                                                                                                                                                    EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 IVQDDDPRVRTTTQPPRGSIPRQSFFNRGHGAPPGGPGPRQQQAGARLGAAQSPFNDLNR
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                                                                                                                           (JUN-1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=7590740; R., Wright C.V.,
                                                                                                                                                                                    islets;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 10;
8; Mismatches
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         Melloul
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Hani E.H., Stoffers D.A., Chevre J.-C., Durand E., Stanojevic V.,
Ab han C., Habbener J.F., Froguel P.;
The pefective mutations in the insulin promoter factor-1 (IPF-1) gene in
RT Tate-onset type 2 diabetes mellitus.";

Clin. Invest. 104:R41-R48(1999).

J. Clin. Invest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macfarlane W.M., Frayling T.M., Ellard S., Evans J.C., Allen L.I., Bulman M.P., Ayres S., Shepherd M., Clark P., Millward A., Demaine A., Wilkin T., Docherty K., Hattersley A.T.; Wissense mutations in the insulin promoter factor-1 gene predispose to type 2 diabetes.";
CONCENTRATION.

-!- DISEASE; Defects in IPF1 are a cause of pancreatic agenesis (MIM:260370). This autosomal recessive disorder is characterized by absence or hypoplasia of pancreas, leading to early-onset insulin-dependent diabetes mellitus. This was found in a frameshift mutation that produces a truncated protein and results in a second initiation that produces a second protein that act as a dominant negative mutant.

-!- DISEASE: Defects in IPF1 are a cause of susceptibility to noninsulin-dependent diabetes mellitus (NIDDM) (MIM:12883); also known as diabetes mellitus type II.

-!- DISEASE: Defects in IPF1 are the cause of maturity onset diabetes of the young type IV (MODY4) (MIM:60392); also symbolized MODY-IV. MODY4 is a form of non-insulin-dependent diabetes mellitus (NIDDM) characterized by an autosomal dominant mode of inheritance, age of onset of 25 years or younger and a primary defect in insulin secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to type 2 diabetes.";
J. Clin. Invest. 104:R33-R39(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cohen P., Docherty K.;
"The p38/reactivating kinase mitogen-activated protein kinase cascade mediates the activation of the transcription factor insulin upstream factor 1 and insulin gene transcription by high glucose in pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Pancreatic islets;
MEDLINE=97400587; PubMed=9252422;
Macfarlane W.M., Smith S.B., James R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [5]
SEQUENCE FROM N.A.
Findner T.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20015026; PubMed=10545531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20015025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: The homeodomain, which contains the nuclear localization signal, not only mediates DNA-binding, but also acts as a protein-protein interaction domain for TCF3 (B47), NEUROD1 and HWG-I(Y) (By similarity).

PTM: PHOSPHORYLATED BY THE SAPK2 PATHWAY AT HIGH GLUCOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chem. 272:20936-20944(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10545530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clifton A.D., Doza Y.N.,
                                                                                                                     R PRINTS; PRO0025; ANTENNAPEDIA.

R PRINTS; PRO0025; ANTENNAPEDIA.

R PRINTS; PRO0021; HOMEOBOX.

R PRINTS; PRO00031; HTHREPRESSR.

R PRODOM; PD000010; HOMEOBOX; 1.

R SMART; SM00389; HOX; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00032; ANTENNAPEDIA; FALSE NEG.

R PROSITE; PS00032; ANTENNAPEDIA; FALSE NEG.

R PROSITE; PS00032; ANTENNAPEDIA; FALSE NEG.

Nuclear protein; Developmental protein; Disease mutation;

W Diabetes mellitus; Phosphorylation; Polymorphism.

TRANSACTIVATION DOMAIN (BY SIMILA)
        Query Match
Best Local Sim
Matches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U35632; AAA88820.1; -.
EMBL; S82178; AAB47101.1; JOINED.
EMBL; S82168; AAB47101.1; JOINED.
EMBL; U30329; AAA74012.1; -.
EMBL; U30329; AAA74012.1; -.
EMBL; AF0035260; AAB88463.1; -.
EMBL; AF0035260; AAB88463.1; JOINED.
EMBL; AF0049893; AAC05157.1; -.
PIR; G01926; G01926.
HSSP; P02833; PANT.
TRANSFAC; T04362; -.
Genew; HGNC:6107; IPF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 600733; ...
MIM; 260370; ...
MIM; 12653; ...
MIM; 12653; ...
MIM; 606392; ...
GO; GO:0003704; F:specific RNA polymerase II transcription fa.
GO; GO:0006091; P:energy pathways; TAS.
GO; GO:0007397; P:histogenesis and organogenesis; TAS.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001827; HTH lambrepressr.
Pfam; PF00046; homeobox; 1.
                                                                                                               CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this, statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SITE
                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPF1/XLHBOX8 SUBFAMILY
                                       Similarity
                                                                                                               56
116
210
283 AA;
           Conservative
                                                                                                                                                                                                                                                                                                   197
                                                                                                               56
116
211
211
30771 MW;
                                                                                                                                                                                                                                                                                                   197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219
244
18
                                                                                                                                                                                                                                                243
                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                 10.9%;
27.7%;
                                                                                                                                           POLYMORPHISM).

/FTIGAVAR 009311.

R -> H (IN MODY4).

/FTIGAVAR 009312.
P -> PP (IN MODY4).
/FTIGAVAR 009313.
A -> S (IN REF. 6).
Q -> H (IN REF. 6).
GG -> SS (IN REF. 6).
        Score 69; DB 1; Length 283; Pred. No. 14; 7; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_009310.
D -> N (IN MODY4; COULD
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C -> R (IN
/FTId=VAR_
                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR 009309.
Q -> L (IN MODY4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION SIGNAL SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTP-TYPE HEXAPEPTIDE
                                                                                                                     5D48EC8D3289F72B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IN MODY4).
                                                                                                                                                    REF. 6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL outstation
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                28;
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L_MESAU
IPF1_MESAU
P70118;
   DOMAIN
DOMAIN
                                               PROSITE; PS00027; HOMEOBOX 1; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.

PROSITE; PS00032; ANTENNAPEDIA; FALSE NEG.

Transcription regulation; Activator; DNA-binding; Homeobox;
                                                                                                                                                                                                                                                                                                      EMBL; U73854; AAB18252.1; -. HSSP; P02833; 9ANT. TRANSFAC; T04267; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rudnick A., Ling T.Y., Odagiri H., Rutter W.J., German M.S.;
Submitted (CCT-1995) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Activates insulin and somatostatin gene transcription.
Key regulator of islet peptide hormone expression but also responsible for the development of the pancreas, most probably by determining maturation and differentiation of common pancreatic precursor cells in the developing gut. Binds the DNA sequence 5'-CC[CT]TAATGGG-3' (By similarity).
-!- SUBCCLLULAR LOCATION: Nuclear (By similarity).
-!- TISSUE SPECIFICITY: Pancreas; islet beta-cells (By similarity).
-!- DOMAIN: The Autp-type hexapeptide mediates heterodimerization of IPF1 with PBX on a regulatory element of the somatostatin promoter
                                                                                                                                                                PRINTS; PR00025; ANTENNAPEDIA PRINTS; PR00024; HOMEOBOX. PRINTS; PR00031; HTHREPRESSR.
                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                   ProDom; PD000010;
SMART; SM00389; HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Insulin promoter factor 1 (IPF-1) (Homeodomain protein PDX1).
IPF1 OR PDX1.
Nuclear protein.
DOMAIN 13
DOMAIN 42
                                                                                                                                                                                                                                    IRANSFAC; T04267; -.
InterPro; IPR001827; Antennapedia.
InterPro; IPR0001356; HTM_lambrepressr.
InterPro; IPR000047; HTM_lambrepressr.
                                                                                                                                                                                                                                Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein interaction domain for TCF5(B4/), NEUROUS SIMILARITY: BELONGS TO THE ANTH HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: The homeodomain, which contains the nuclear localization signal, not only mediates DNA-binding, but also acts as a protein-protein interaction domain for TCF3(E47), NEUROD1 and HMG-I(Y) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPF1/XLHBOX8 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 LEEP----NR---VQLPFPWMKSTKAHAWKGQWAGGAYAAEP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQSPFNDLNRQLVNMGFP-----OWHLGNHAVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALGALEQGSPPDISPYEVPPLADDPAVAHLHHHLPAQLALPHPPAGPFPE----GAEPGV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANGEIVQDDDPRVRTTTQPPRGSIPRQSFFNRGHGA-----PPGGPGPRQQQAGARLGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                 HOX; 1.
                                                                                                                                                                                                          ANTENNAPEDIA.
                                                                                                                                                   Homeobox; 1.
   73
48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Cricetinae;
TRANSACTIVATION DOMAIN (BY SIMILARITY). POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Å
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                                                                                                               SPREE
                                                                          Query Match
Best Local S
Matches 24
                                                                                                               DOMAIN
SEQUENCE
                                                                                                                                          SITE
DNA BIND
DOMAIN
113 SRGQLPFPWMKSTKAHAWKGQWAGGAYAVEP 143
                  58 GAAQSPENDLNRQLVNMGFPQWHLGNHAVEP
                                     53 ALGTLEOGSPPDISPYEVPPLAEDPAVAHLHHHLPAQLGLAHPPSGPFPNGTEPGGLEEP
                                                   6 ANGEIVQDDDPRVRTTTQPPRGSIPRQSFFNR-----GHGAPPGGPGPRQQQAGA--RL
                                                                          24;
                                                                           Similarity 26.4
24; Conservative
                                                                                                              239
283 AA;
                                                                                                                                           118
146
197
                                                                                                                        244
                                                                                                                                          205
                                                                                                               30819 MW;
                                                                                   10.9%;
                                                                          8; Mismatches
                                                                                   Score 69;
Pred. No.
                                                                                                             SIMILARITY).
POLY-PRO.
; 22714BB5AED54BF2 CRC64;
                                                                                                                                          ANTP-TYPE HEXAPEPTIDE. HOMEOBOX. NUCLEAR LOCALIZATION SIGNAL
                                                                                            BB
                  88
                                                                                            ۲,
                                                                        51;
                                                                                            Length 283;
                                                                          Indels
                                                                                                                                            (BY
                                                                         8
                                                                         Gaps
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2; 57 112

Search completed: August 24, 2004, 09:18:24 Job time : 12 secs

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein -
       8
                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                           632
568.5
110.5
110.9
99.5
83.5
82
82
82
82
82
87
                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                             SPTREMBL 25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_funer:*
5: sp_invertebrate
6: sp_mammal:*
6: sp_macmal:*
8: sp_organelle:*
9: sp_bage:*
10: sp_plant:*
11: sp_viens:*
12: sp_viens:*
13: sp_vertebrate
                                                                                                                                                                                              Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     August 24, 2004, 09:17:04 ; Search time 40 Seconds (without alignments) 954.443 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-001-885-125
632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVRILANGEIVQDDDPRVRT......GVRGLLLVGLVYLVSHLSQR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                          sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                               sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_archeap:*
                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                      invertebrate:*
                                     121
120
131
132
132
223
223
219
174
102
608
475
392
717
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12
12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1017041
Q96d05 homo sapien
Q9d802 mus musculu
Q9c212 mus musculu
Q9c215 nus musculu
Q8n8j7 homo sapien
Q8tb5 streptomyce
Q9nt75 homo sapien
Q8xrn3 oryza sativ
Q3x694 heppatitis d
Q9q5k9 herpesvirus
Q9q5k9 herpesvirus
Q9q5k9 herpesvirus
Q9q5k9 mus musculu
Q7ug24 rhodopitell
Q3d518 heppatitis d
Q39945 heppatitis d
Q39945 heppatitis d
                                                                                                                                                                                              Description
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5	44	43	42	41	40	39	38	37	36	35	34	IJ ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
•	73.5	•	•	74	74	74	74	74	74	74	74.5	74.5	74.5	75	75	75	75	76	76	76	76	76	76	76	76		76.5		
11.6		11.6	11.6	•	11.7	11.7	11.7			11.7			•	11.9	•	•		•	12.0		٠	•	12.0	•	•	•	12.1		
332	254	195	81	1794	1260	899	588	256	214	102	1151	1003	426	701	102	102	102	717	717	395	252	252	204	140	102	1201	214	692	
11							4.	N	12	12	1	υı	N	4.	12	12	12	<u>بر</u>	11	11	4					16	12	υı	
Q9D7D1	Q9N357	Q9E924	Q912E0	P87515	Q9UGY9	Q881Q1	Q9BW18	Q9F5M2	Q9E925	036121	Q9Z0F2	Q9W326	087638	Q8N1X3	036128	036153	036127	Q8C7W4	Q9CXJ4	Q8BYS2	QBIXI8	Q9NX53	013598	Q9DCP6	036114	Q9HU70	9	Q19579	
Q9d7d1 mus musculu	Q9n357 caenorhabdi	hepatiti	Q912e0 hepatitis d	barmah f	Q9ugy9 homo sapien	pse	omo sap	Q9f5m2 rhodocyclus	Q9e925 hepatitis d	O36121 hepatitis d	Q9z0f2 mus musculu	Q9w326 drosophila	O87638 pseudomonas	Q8n1x3 homo sapien	hepa	036153 hepatitis d	hepa	Q8c7w4 mus musculu	Brim	62 mus		homo	zosaccì	5 mus muscul	O36114 hepatitis d	pseudomona	999v2	Q19579 caenorhabdi	

ALIGNMENTS

ď	8	뭥	β	뭥	Ş	M H Q	SO	3 5	R.	RC	RP	말 X	8	88	בי מ	ij	DT	D A	ij,	RESULT	
121 R 121	121 R 121	61 QSPRIDLNRQLVNMGFPQWHLGNHAVEPVTSILLLFLLMMLGVRGLLLVGLVYLVSHLSQ 120	61 QSPFNDLNRQLVNMGFBQWHLGNHAYEPVTSILLLFILMMLGVRGLLLVGLVYLVSHLSQ 120	1 MVRILANGEIVQDDDPRVRTTTQPPRGSIPRQSFFNRGHGAPFGGFGFRQQQAGARLGAA 60	1 MVRILANGEIVQDDDPRVRTTTQPPRGSIPRQSFFNRGHGAPPGGFGRRQQQAGARLGAA 60	Query Match 100.0%; Score 632; DB 4; Length 121; Best Local Similarity 100.0%; Fred. No. 1e-60; Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps	SEQUENCE 121 AA; 13238 MW; 6326728CAB5375C4 CRC64;			TISSUE=Pancreas;	SEQUENCE FROM N.A.	NCBI_TaxID=9606; [1]	ia; Primates; Catarrhini; Hominidae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	SIMILIAT TO KIKEN CUNA ZOIDIU/GZ3 gene.		(TrEMBLrel. 19,	Q96D05; 01-DEC-2001 (TrEMBLrel. 19, Created)	Q96D05 PRELIMINARY; PRT; 121 AA.	DOS	
		ŏ	õ	٥	_	0;															

RESULT 2 Q9D882

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ACCOMPARATE AND DESCRIPTION OF THE PROPERTY OF
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Best Local Similarity
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"Analysis of the mouse transcriptome based on functional annote
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK008338; BAB25613.1; --
EMBL; BK024943; BAB25613.1; --
EMBL; BK035688; BAC29152.1; --
EMBL; AK035688; BAC29152.1; --
EMBL;
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Mammalia; Eutheria;
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01-MAR-2003 (TrEMBLrel. 23, L
2010107G23Rik protein (RIKEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21085660; PubMed=11217851;
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SEQUENCE 120 AA; 1
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                                                                                                                                                          QSPFNDLNRQLVNMGFPQWHLGNHAVEPVTSILLFLLMMLGVRGLLLLVGLVYLVSHLSQ
                                                                                     QSPFSDLNRQLVNMGFPQWHLGNHVVBPVTSILLLFLLMMLGVRGLLLVGLVYLVSHLSQ
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Rodentia;
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17,
23,
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Sciurognathi; Muridae; Murinae; Mus
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RA Kawai J., Shinagawa A., Shibata K., Komon H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Komon H., Adachi J., Fukuda S.,
RA Airawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Airawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov G., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carminci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Myoshaw H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Myoshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashizaki Y..
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01-JUN-2001
01-MAR-2003
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation updat
Hypothetical protein FLJ39370.
Homo sapiens (Human).
    Oshima A., Takahashi-Fujii A.,
Arita M., Musashino K., Yuuki I
Otsuki T., Sato H., Wakamatsu i
Kawai-Hio Y., Saito K., Nishik
Matsuo K., Nakamura Y., Sekine
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5730508B09RIK OR 2700063A17RIK.
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria;
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Takahashi-Fujii A., Tanase T., Imose N., Takeuchi
Musashino K., Yuuki H., Hara H., Sugiyama T., Irie
Sato H., Wakamatsu A., Ishii S., Yamamoto J., Ison
Y., Saito K., Nishikawa T., Kimura K., Yamashita H.
Nakamura Y., Sekine M., Kikuchi H., Kanda K., Waga
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Pred. No. 5.3e
19; Mismatches
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Best Local Similarity
                                                                                                                             Q82HR5;
Q82HR5;
Q1-JUN-2003
01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ
EMBL; BC022534; AAH22534.1; -.
Hypothetical protein.
SEQUENCE 132 AA; 14787 MW; 284B5499A1E50F(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002
01-JUN-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSTBF9;
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahash
                                                        Streptomycineae; NCBI_TaxID=33903;
                                                                                 Streptomyces avermitilis. Bacteria; Actinobacteria;
                                                                                                           Hypothetical SAV3443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. Homo sapiens (Human).
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                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                l Similarity
27; Conserv
                                                                                                                                                                                                                                                              HAVEPVISILLLFLLMMLGVRGLLLVGLVYLV 115
                                                                                                                                                                                                                                                                                                          PGPROQQAGARLGAAQSP------FNDLNRQLVNMGFPQWHLGN
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31.9%;
                                                                                  Actinobacteridae; Actinomycetales;
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Pred. No. 0.00039;
7; Mismatches 34;
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Mismatches 29
                                                                     Streptomyces.
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T.;
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RESULT 7
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RESULT
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Best Local S
Matches 29
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Best Local S
Matches 23
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Q9NT75,
01-077-2000 (TrEMBLrel. 15, Createu,
01-077-2000 (TrEMBLrel. 15, Last sequence update,
01-077-2000 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
----hetical protein (Fragment).
  Q7XRN3
Q7XRN3;
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EMBL; AL137488; CAB70767.1; -.
PIR; T46472; T46472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
EMBL; AP005035; BAC71155.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
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MEDLINE=22608306; PubMed=12692562;
NEdda H., Ishikawa J., Hanamoto A., Shinose M., Kikuch
Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                    APPGGPGPRQQQAGARLGAAQSPFNDLNRQLVNMGFPQWHLGNHAVEPVTSILLLFLLMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 AA; 24989 MW;
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223 AA; 23128 MW; AF13F56F4FDB9A87 CRC64;
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                                                                                                                                                                                                                                                                                                                                                       Conservative
                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                           13.2%;
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                                                                                                                                                                                                                                                                                                                                                  Score 83.5; D
Pred. No. 0.6;
11; Mismatches
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Pred. No. 0.011;
9; Mismatches 21;
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                              PRT;
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Matches 27
                Query Match
Best Local S
Matches 25
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Li Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
Submitted (MAY-2002) to the EMEL/GenBank/DDBJ databases.
EMEL, AL731596; CAEC2411.1;
SEQUENCE 174 AA, 17749 MW; 6BD95E3BD5117DC7 CRC64;
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036094;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
[1]
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
OSJNBA0024722.19 protein.
Oryza sativa (Rice).
                                                                                                                                                ProDom; F
NON TER
SEQUENCE
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STRAIN-Turkish isolate 07;

MEDIINE=973708276, PubMed=9234957;

MEDIINE=973708276, PubMed=9234957;

Shakil A.O., Hadziyannis S., Hoofnagle J.H., Di Bisceglie A.M.,

Schain J.L., Casey J.L.;

"Geographic distribution and genetic variability of hepatitis di

Virus genotype I.";

Virology 234:160-167(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hepatitis delta antigen (Fragment).
Hepatitis delta virus (HDV).
Viruses; Deltavirus.
                                                                                                                                                                                                                                                                                                       EMBL; ĀF008349; AAB66964.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
                                                                                                                                                                                                                                          InterPro; IPR002506; HDV_ag. Pfam; PF01517; HDV_ag; 1.
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                    l Similarity
25; Conserv
                                                                                                                                                                                                     F01517; HDV_ag; 1.
PD002887; HDV_ag; 1.
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                13.0%;
nilarity 32:9%;
Conservative 10
                                                                                                                                                102 AA;
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                                                                                                                                                11085 MW;
                       10;
                       Score 82; DB
Pred. No. 0.36
10; Mismatches
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                                                                                                                                                   3136BB4EA439F792 CRC64;
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                                                                                   DB 12; Length 102;
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                          27;
                          Indels
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                              14;
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AC 0905K
AC 0905K
DT 01-MA
DT 01-OC
DE NTR.
OS Herbe
OC Virus
OC Gamma
OC Gamma
OC NCBI
RN [1]
RN [1]
RR 2009
RA ZONG
RA ZONG
RA Haywa
SQ SEQUE
Q9A913
ID Q9A91
AC Q9A91
AC Q9A91
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-GC
DE SCHEG
GN CC118
CC118
COC Caulo
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RC STRAINARTCC 19089 / CB15;

RX MEDIANE-21173698; PubMed=11259647;

RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

RA Nierman W.C., Feldblyum T.V., Laub M.R.K., Ohta N., Maddock J.R.,

RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA Potocka I., Nelson W.C., Newton A., Stophens C., Phadke T., Ely B.,

RA Clonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Kolonay J.F., Venter J.C., Shapiro I., Fraser C.M.,

"Complete genome sequence of Caulobacter crescentus.";

PTOC. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

"PTOC. NATL. Acad. Sci. U.S.A. 98:4136-4141(2001).

"COMPLETE SENSORY TRANSDUCTION PROTEINS.

EMBL; AB005795; AAK23165.1; -.

DR GO; GO:0016301; F:kinase activity; IEA.

DR GO; GO:0016301; F:kinase activity; IEA.

DR GO; GO:0016301; F:kinase activity; IEA.
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01-MAY-2000
01-MAY-2000
01-OCT-2002
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
Sensor histidine kinase.
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STRAIN-Baboon lymphocryptovirus BA65;

ZONG J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S.,

Rayward G.S.;

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

SEMBL, AF20364; AAF23950.1;

SEQUENCE 608 AA; 60458 MW; 4BF82ACB0A029627 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ATCC 19089
MEDLINE=21173698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caulobacter crescentus.
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
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ilarity 47.4%;
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(TrEMBLrel. 22, Last ann
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Pfam; PF02518; HATPase C; 1.

Pfam; PF02512; HisKA; 1.

PRINTS; PR00344; BCTRLSENSOR.

SMART; SM00304; HAMP; 1.

SMART; SM00387; HATPase C; 1.

SMART; SM00388; HisKA; 1.
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Q82JY1;
Q1-JUN-2003
Q1-JUN-2003
Q1-OCT-2003
 연 (00)
연 (05)
TABMET /
                                                                                                                                                                            STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
Omura S., Tkeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
metabolites.";
                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative phosphatidate cytidylyltransferase.
CDSA OR SAV2623.
                                       "Complete genome sequence and comparative analysis microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
                                                                                                           SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIM
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                               Proc.
                                                                                                                                                                                                                                                                                                                                Streptomyces avermitilis.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                 Ikeda H., Ishikawa J., Hanamoto . Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0007600; P:sensory perception; I GO; GO:0007165; P:signal transduction; InterPro; IPR003594; ACT sens_pr_C. InterPro; IPR004358; Bact_sens_pr_C. InterPro; IPR003660; HAMP. INTERPRO; IPR003661; His kinase. InterPro; IPR003661; His kinase. InterPro; IPR003661; His kina.N.
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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PROSITE; PS50109; HIS KIN; 1.

Kinase; Phosphorylation; Sensory transduction; Transferase;
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L; AP005031; BAC70334.1; -. GO:0016020; C:membrane; IEA. GO:0004605; F:phosphatidate
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                                                                                                                                                                 Acad. Sci. U.S.A.
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           IEA.
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Pred. No. :
                                                                                                                                                                 98:12215-12220(2001)
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cytidylyltransferase
                                                                                              Shinose M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         392
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2.7;
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                                                                                              Kikuchi H.,
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activity;
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Н.,
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Best Local S
Matches 37
                                                                                          Matches
                                                                                                                Query Match
Best Local :
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EMBLY AK076315; BAC36297.1; ...
MGD; MGI:1921860; 4833412NOZRİK.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0000166; F:nuCl-binding cassette (//
GO; GO:0000166; F:nuCl-binde binding; IEA.
GO; GO:0000166; F:nuCl-binde binding; IEA.
GO; GO:0000166; F:nuCl-binde binding; IEA.
                                                                                                                                                                                                        ProDom; PD000006; ABC
SMART; SM00382; AAA; I
PROSITE; PS00211; ABC
PROSITE; PS50893; ABC
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InterPro; IPR001140; ABC TM_transpt.
InterPro; IPR003439; ABC transporter.
Pfam; PF00664; ABC membrane; 1.
Pfam; PF00005; ABC tran; 1.
ProDom; PD000006; ABC transporter; 1.
SMART; SM00382; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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GO; GO:0008654; P:phospholipid biosynthesis; IEA.
InterPro; IPR000374; PC trans.
Pfam; PF01148; CTP transf_1; 1.
PROSITE; PS01315; CDS; 1.
SEQUENCE 392 AA; 40876 MW; C6F6A4254E7CBAC6 CRC64;
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ATP-binding cassette.
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01-MAR-2003 (TremBLrel.
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                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
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MEDLINE=223546B3; PubMed=12466851;
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                                                                                                                Similarity
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                                                                                                                                                                                  PS00211; ABC_TRANSPORTER_1; 1.
PS50893; ABC_TRANSPORTER_2; 1.
717 AA; 77983 MW; 72CC6DE60C967755
GAALVNVQIPL--LLGQLVEMVAKYTRDHMGSFVSE--SRXLSVQLLLLYGVQGLLTFGY
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                                           GARLGAAQSPFNDLNRQLVNM--GFPQWHLGNHAVEPVTSILLLFLLMMLGVRGLLLVGL
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Last annotation update)
                                                                                       Score 80; DB:
Pred. No. 5.6;
L3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transporter
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
R38177.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heparitis delta antigen (Fragment).
Hepartiis delta virus (HDV).
Viruses; Deltavirus.
Shakil A., Hadziyannis S., Hoofnagle J.H., DiBisceglie A.M., Gerin J.L., Casey J.L., Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

EMBI ADD08420 ABR57015 1 -
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Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
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Planctomycetaceae; Pirellula.
MCBI_TaxID=117;
                                                                                                                                                                                    Casey J.L.;
"The predominance of hepatitis delta virus genotype I among chronically infected Italian patients.";
Hepatology 25:728-734(1997).
                                                                                                                                                                                                                                                                                                            MEDLINE=97201440; PubMed=9049226;
Niro G.A., Smedile A., Andriulli A., Rizzetto M., Gerin J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome.
SEQUENCE 1318 AA; 148033 MW; 502BC65297DB7F04 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=12475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1135 DEEPSTEPTPGEPSENTEPQESTERPQGPPGLRPSSQSQQQQQPQPNQPQEGQSGGPNPSA 1194
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5 LVLLSHIGER 204
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ilarity 28.7%;
Conservative
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Pred. No. 17
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Search completed: August 24, 2004, 09:19:11 Job time : 45 secs
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Matches 24;
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InterPro; IPR002506; HDV ag.
Pfam; PF01517; HDV ag; 1.
ProDom; PD002887; HDV ag; 1.
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Similarity 30.0%; Pred. No. 0.97;
24; Conservative 10; Mismatches 26; Indels
                                                                                      NDLNRQL --- VNMGFPQWHL 81
                                                                                                                      KLTEEDERRERRVAGPPAGGV-----NPLEGAPRGAPGGGFVPSMO-----GVPESPF
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptcdatta/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdatta/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/iaa/backfIles1.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-621-976-4724
US-09-149-476-673
US-09-149-476-6924
US-09-621-976-6924
US-09-252-991A-23015
US-09-252-991A-25310
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US-09-252-991A-25276
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US-09-252-991A-33130
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US-09-252-991A-234364
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Sequence 23015, A
Seguence 23015, A
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ALIGNMENTS

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Sequence 4724, Application US/09621976
; Sequence 4724, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILLING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4724
; LENGTH: 104
; TYPE: PRT
US-09-621-976-4724
                                                                                                                                                                                                                                   Sequence 673, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
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US-09-149-476-673
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US-09-621-976-4724
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Best Local Similarity 100
Matches 104; Conservative
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ER APPLICATION NUMBER: 60/047,581
ER APPLICATION NUMBER: 60/047,584
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,584
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,580
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,492
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,598
ER APPLICATION NUMBER: 60/047,613
ER APPLICATION NUMBER: 60/047,613
ER APPLICATION NUMBER: 60/047,582
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,582
ER APPLICATION NUMBER: 60/047,582
ER APPLICATION NUMBER: 60/047,596

ER APPLICATION NUMBER: 60/047,617
ER FILLING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,618
ER FILLING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,503
ER FILLING DATE: 1997-05-23

APPLICATION NUMBER: 60/047,592 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,633 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,583 FILING DATE: 1997-05-23 FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/047,600
FILING DATE: 1997-05-23

APPLICATION NUMBER: 60/047,615 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,597 FILING DATE: 1997-05-23

APPLICATION NUMBER: 60/047,502 FILING DATE: 1997-05-23

FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,626
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,334
FILING DATE: 1997-03-07

APPLICATION NUMBER: 60/040,336 FILING DATE: 1997-03-07

APPLICATION NUMBER: 60/040, 163

ER APPLICATION NUMBER: 60/043,674
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,669
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,312
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,313
ER FILING DATE: 1997-04-11

ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,568
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,314
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,569
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,311
ER APPLICATION NUMBER: 60/043,671
ER APPLICATION NUMBER: 60/043,671
ER FILING DATE: 1997-04-11
ER FILING DATE: 1997-04-11

PRILING DATE: 1997-05-23
RAPPLICATION NUMBER: 60/047,612
RRILING DATE: 1997-05-23
RR APPLICATION NUMBER: 60/047,632
RR FILING DATE: 1997-05-23
RR APPLICATION NUMBER: 60/047,601

FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580

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RESULT 3
US-09-149-476-367
; Sequence 367, App
; Patent No. 64205;
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Best Local S
Matches 73
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ00ZP1
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     CURRENT CURRENT EARLIER ILE REFERENCE: PZ002PI

FRRENT FALING DATE: 1998-09-08

RRIER FILING DATE: 1998-09-08

RALIER APPLICATION NUMBER: PCT/US98/04493

RALIER FILING DATE: 1998-03-06

RALIER FILING DATE: 1997-03-07

RALIER PILING DATE: 1997-03-07

RALIER APPLICATION NUMBER: 60/040,333

RALIER PILING DATE: 1997-03-07

RALIER APPLICATION NUMBER: 60/040,626

RALIER APPLICATION NUMBER: 60/040,626

RALIER PILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/0
APPLICATION 1997-08-22
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APPLICATION NUMBER: 6
FILING DATE: 1997-08-
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/
FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/056,862
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/049,610
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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ER APPLICATION NUMBER: 60/047,582
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,612
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,612
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,601
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/043,580
ER APPLICATION NUMBER: 60/043,580
ER APPLICATION NUMBER: 60/043,568
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,314
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ER APPLICATION NUMBER: 60/043,671
ER APPLICATION NUMBER: 60/043,674
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,669
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ER APPLICATION NUMBER: 60/047,618
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,503
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ER APPLICATION NUMBER: 60/047,581
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ER APPLICATION NUMBER: 60/047,584
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ER APPLICATION NUMBER: 60/047,500
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ER APPLICATION NUMBER: 60/047,587
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FILLNG DATE: 1997-03-07
APPLICATION NUMBER: 60/040,336
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,583
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,502
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,617
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/048,974
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/056,886

FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-08-22

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RESULT 4
US-09-621-976-6924
; Sequence 6924, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
APPLICANT: Dumes Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Pro
FILE REFERENCE: GENEET. 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT APPLICATION SET: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6924
; LENGTH: 113
; TYPE: PRT
ORGANISM: Homo sapiens
; FEATURE:
, NAME/KEY: UNSURE
; LOCATION: 97
; OTHER INFORMATION: Xaa =
US-09-621-976-6924
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ER FILING DATE: 1997-08-22
ER APPLICATION NUMEER: 60/056,881
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,909
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,875
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,862
ER APPLICATION NUMBER: 60/056,962
ER APPLICATION NUMBER: 60/056,908
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,908
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,964
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/057,650
ER FILING DATE: 1997-09-05
ER APPLICATION NUMBER: 60/057,669
ER FILING DATE: 1997-09-05
ER APPLICATION NUMBER: 60/057,669
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ER APPLICATION NUMBER: 60/057,669
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ER FILLING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/056,632
ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,664
ER FILLING DATE: 1997-08-22
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/047,501
FILING DATE: 1997-05-23
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Pred. No. 1.3e-21;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 48,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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EARLIER
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ER APPLICATION: NUMBER: 60/056,888
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,879
ER APPLICATION NUMBER: 60/056,880
ER APPLICATION NUMBER: 60/056,894

FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,911
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,636
FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,878
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,662
ER APPLICATION NUMBER: 60/056,872
ER APPLICATION NUMBER: 60/056,872
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,637
ER APPLICATION NUMBER: 60/056,637
ER APPLICATION NUMBER: 60/056,637
ER APPLICATION NUMBER: 60/056,903
ER APPLICATION NUMBER: 60/056,903
ER APPLICATION NUMBER: 60/056,903
ER APPLICATION NUMBER: 60/056,903

ER APPLICATION NUMBER: 60/056,889
ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,893
ER FILLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,630
ER FILLING DATE: 1997-08-22

EARLIER

APPLICATION NUMBER: 60/047,614 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,578 FILING DATE: 1997-04-11

Ouery Match
Ouery Match
Best Local Similarity 83.9%; Pred. No. 1.6e-20;
Matches 47; Conservative 1; Mismatches 6;

Length 113;

Indels

ER APPLICATION NUMBER: 60/047,599
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,588
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,585
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,586
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,590
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,590
ER APPLICATION NUMBER: 60/047,594
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,589
ER APPLICATION NUMBER: 60/047,593

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EARLIER

ER APPLICATION NUMBER: 60/056,874

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,910

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,864

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,631

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,845

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,892

ER APPLICATION NUMBER: 60/057,761

ER APPLICATION NUMBER: 60/047,595

ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,595

ER FILING DATE: 1997-05-23

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RESULT 7
US-08-889-402-2
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                                                                                                                                                                                                                                                    ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-30146
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US-09-489-039A-8966
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8966
LENGTH: 1999-01-29
Sequence 2, Application US/08889402
                                                                                                                                                                                                                                                                                                              SEQ ID NO 30146
LENGTH: 763
                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30146, A
Patent No. 655179
                                                                                                                                                                             Matches
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Best Local :
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Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SECID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gary Breton et. al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 460
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 22; Conserv
                                                                                                    443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213
                                                                                                                                  12 QDDDPRVRTTTQPPRGSIPRQSFFNRGHGA----PPGG--PGPRQQQAGARLGAAQSP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 RIGAAQSPFNDLNRQLVNM-GFPQWHLGNHAVEPVTSILLLFLLMMLGVRGLLLVGLVYL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43
                                                                                                                                                                           l Similarity 39.0
23; Conservative
                                                                                                 QGGDGRPRPTDERRAGATPGQAL--RAQGAPAGTLPPGGRAHGPRRQPAGGRRAGPEHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPVWLSNMSE 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.9%; Score 88; DB 4; Length 460. ilarity 31.4%; Pred. No. 0.052; Conservative 17; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09252991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107196.136
                                                                                                                                                                                           12.6%;
                                                                                                                                                                         Score 79.5; DB Pred. No. 0.99; 5; Mismatches
                                                                                                                                                                                                            DB 4;
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                                                                                                                                                                                                              Length 763;
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF ESG ID NOS: 33142
SEQ ID NO 23015
LENGTH: 217
                                                                                                                                                                                  ; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-23015
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US-09-252-991A-23015
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                                                                                                         Query Match
Best Local S
Matches 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 17:
PILLING DATE: 08-JUL-1996
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELAT
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: NOVI
TITLE OF INVENTION: PRO/
NUMBER OF SEQUENCES: 7
COMPUTER REALDABLE FORM:
MEDIUM TYPE: Floppy d:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
CELL TYPE: Monoblastic cell and placenta
CELL LINE: U937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 605 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 AKG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 PSLRSPDQPP----PCPQFMAQGKTGSSSPPGGPPKPGSQLDSMLGSLQSDLNKLGVATV
                                   91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 NMG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 PRVRTTTQPPRGSIPRQSFF---NRGHGAPPGGPGPRQQQAGARLGAAQSPFNDLNRQLV 72
73 NMGFPQWHLG 82
                                                                                                           23;
                                                                                                                               Similarity
                                   RAGVPARS-RRRGHGRPPGMVADRSAGPTAGLPAQPRLHDAGASLPGSDPP
                                                                    RGSIPRQSFFNRGHGAPPG-----GP-----GPRQQQAGARLGAAQSPFNDLNRQLV 72
                                                                                                           Conservative
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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                                                                                                                           12.0%;
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IN PAXILLIN
                                                                                                         3; Mismatches
                                                                                                                           Score 76; DB 4
Pred. No. 0.49;
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Pred. No. 0.96;
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                                                                                                                                           DB 4; Length 217
                                                                                                         18;
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                                                                                                         Indels
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                                                                                                         26;
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US-09-252-991A-25314
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PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107195.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22303
LENGTH: 200
TYPE: NEWTON
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MARC J. Rubenfield et al.

APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25314

LENGTH: 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25314, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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                                                                                                                                                                               Matches
                                                                                                                                                                                                      Query Match
Best Local Similarity
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
-09-252-991A-22303
                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
-09-252-991A-25314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 11.9%; Score 75; DB 4;
Local Similarity 33.3%; Pred. No. 0.58;
hes 22; Conservative 5; Mismatches 2
           58 GAAOSPENDLNROLVNMGFPOWHLGNH 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 GVGQRH 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 DERVETTTQPPEGSIPEQSFFNEGHGAPPGGEGERQQQAGARLGAAQSPFNDLNEQLVNM 74
                                                                                                                                                                               29;
                                                                                                                    3 RILANGEIVQ-DDDPR----VRTTTQPPRGSIPRQSFFNRGHGAPPGGPGPRQQQAGARL 57
                                                                      RIVEQGEVWEVFGDPRHARHPKPVRQPAR------
                                                                                                                                                                                                   11.9%; Score 75; DB 4; Length 655; 33.3%; Pred. No. 2.7;
                                                                                                                                                                               8
                                                                                                                                                                                  Mismatches
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                                                                         -RPPGRPPGAPAPGSRR--RRP 563
                                                                                                                                                                                  Indels
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                                                                                                                                                                                  Gaps
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564 GAARSPVH--RROPTGAG-PAGHROGH 587

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RESULT 13 US-09-252-991A-24325

Sequence 24325, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al.

APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

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RESULT 12
US-09-252-991A-28276
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US-09-252-991A-31559
                                                                                                                                                                                                                                          ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-28276
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APPLICANT: MARC J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MATC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31559
LENGTH: 215
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SEQ ID NO 28276
LENGTH: 263
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                                                                                                             Query Match 11.7%; Score 74; DB 4; Length 263; Best Local Similarity 41.7%; Pred. No. 1.1; Matches 25; Conservative 6; Mismatches 7; Indels
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ASSUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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98 RPPRAALQRSRAGRRARNRPPVLLPGRRAQRLGQRPGAGQNNFN 141
                                                   15 pprvrtttop-----prgsiprosffnrghgappggpgp-----roqqqagar-Lgaaqsp 63
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22026
ENGRH: 270
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US-09-252-991A-32396
        Sequence 32396, Application.

Sequence 32396, Application.

Sequence 32396, Application.

Sevent No. 6551795

Patent No. 65517
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US-09-252-991A-22026
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24325
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 RVRTTTQPP--RGSIPRQSFFNRGHGAPPGGPGPRQQQAGA------RLGAAQSPFN 65
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(1 Similarity 32.1%; Pred. No. 3.9;
26; Conservative 11; Mismatches
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Search completed: August 24, 2004, 09:19:53
Job time : 20 secs
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 32396
LENGTH: 351
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                              104 AHPVGPALRRRGLRRLHLGGRRTHPAWS 131
                                                                                                                     64 FNDLNRQLVNMGFPQWHLGNHAVEPVTS 91
                                                                                                                                                            47 ŔTAPVPARGRRPDQ---RRGSGAPRAGAGEPGPSRPVGDHPEPLRRPATDPAGRDRPQPP 103
                                                                                                                                                                                                   19 RTTTQPPRGSIPRQSFFNRGHGAPPGG---PGP-----RQQQAGARLGAAQSP 63
                                                                                                                                                                                                                                             l Similarity 30.7
27; Conservative
                                                                                                                                                                                                                                        11.6%; Score 73; DB 30.7%; Pred. No. 2.1; ative 3; Mismatches
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                                                                                                                                                                                                                                             Indels
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Title: US-10-001-885-125
Perfect score: 632
Sequence: 1 MVRILANGEIVQDDDPRVRT......GVRGLLLVGLVYLVSHLSQR 121
Scoring table: BLOSUM62

table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1295152 segs, 314255058 residues
Total number of hits satisfying chosen parameters:

1295152

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
632 387 387 245 245 99.5 88.8 81 82.8	Score
100.0 100.0 61.2 61.2 38.8 38.8 117.5 113.5 113.0 12.8	Query
1221 1221 1221 1211 1211 122 122 122 12	Query Match Length
11 12 12 13 14 14 14 14 14	DB
US-10-001-885-125 US-10-076-747-122 US-09-809-391-673 US-09-882-171-673 US-09-809-391-367 US-09-809-391-367 US-09-882-171-367 US-09-882-171-367 US-10-104-861-367 US-10-104-861-367 US-10-104-861-367 US-10-104-969-3882 US-10-425-59174474 US-10-425-514-60982 US-10-106-698-8371 US-10-156-761-10160	ID
Sequence 125, App Sequence 122, App Sequence 673, App Sequence 673, App Sequence 367, App Sequence 367, App Sequence 367, App Sequence 367, App Sequence 367, App Sequence 10980, A Sequence 174474, Sequence 198292, Sequence 60982, Ap Sequence 198292, Sequence 1971, Ap Sequence 10160, A	Description

61

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US-10-425-114-64460 Sequence 6 75.5 11.9 622 15 US-10-240-145-133 Sequence 6 75.5 11.9 701 15 US-10-108-260A-2701 Sequence 2 75.5 11.9 701 15 US-10-108-260A-2701 Sequence 2 75.5 11.5 13.1 15 US-10-3437-963-149016 Sequence 1 72.5 11.5 13.7 16 US-10-437-963-149016 Sequence 2 72.5 11.5 14.0 15 US-10-369-493-18063 Sequence 2 72.5 11.4 125 12 US-10-369-493-18063 Sequence 7 72.1 11.4 125 12 US-10-245-114-70983 Sequence 2 72.5 11.3 195 14 US-10-237-963-183078 Sequence 2 73.5 11.3 195 14 US-10-237-963-1150350 Sequence 2 73.5 11.3 19662 15 US-10-437-963-1150350 Sequence 2 73.5 11.3 19662 15 US-10-437-963-115864 Sequence 1 73.5 11.3 19662 15 US-10-437-963-115864 Sequence 1 74.5 11.3 19662 15 US-10-084-84A-6 Sequence 2 75.5 11.2 14.0 12 US-10-25-386-32918 Sequence 2 75.5 11.2 14.0 12 US-10-25-386-32918 Sequence 2 75.5 11.2 248 12 US-10-25-3929-105 Sequence 3 75.5 11.2 248 12 US-10-25-3929-105 Sequence 3 75.5 11.2 248 12 US-10-424-599-231854 Sequence 3 75.5 11.2 248 12 US-10-425-114-42547 Sequence 2 75.5 11.2 248 13 US-10-29-386-32918 Sequence 3 75.5 11.2 248 13 US-10-29-386-32918 Sequence 3 75.5 11.2 248 13 US-10-425-114-42547 Sequence 2 75.5 11.2 248 13 US-10-425-114-42547 Sequence 1 75.5 11.2 248 13 US-10-437-963-118692 Sequence 1 75.5 11.2 1734 16 US-10-437-963-118692 Sequence 1 75.5 11.2 1734 16 US-10-437-963-118692 Sequence 1 75.5 11.2 1734 16 US-10-437-963-118692 Sequence 2 75.5 11.2 1734 16 US-10-437-963-118692 Sequence 1 75.5 11.3 175.5 11.3 11.3 11.5 US-10-437-963-118692 Sequence 1 75.5 11.3 11.3 11.5 US-10-437-963-118692 Sequence 1 75.5 11.3 11.3 11.5 US-10-437-963-118692 Sequence 2 75.5 11.5 11.3 11.5 US-10-437-963-118692 Sequence 1 75.5 11.5 US-10-437-963-118692 Seq	76.5 12.1 2246 16 US-10-437-963-164016 Sequence 0 76.5 12.1 2246 16 US-10-425-114-64460 Sequence 0 17.5 11.9 622 15 US-10-426-145-133 Sequence 0 17.5 11.9 622 15 US-10-108-260A-2701 Sequence 2 75 11.9 701 15 US-10-437-963-149016 Sequence 2 75 11.6 236 16 US-10-437-963-149016 Sequence 2 75 11.5 13.7 16 US-10-437-963-149016 Sequence 1 17.5 11.5 13.7 16 US-10-437-963-149016 Sequence 1 17.5 11.3 13.6 16 US-10-437-963-183078 Sequence 2 71.5 11.3 13.3 19.5 14 US-10-425-114-40428 Sequence 2 71.5 11.3 13.6 16 US-10-437-963-183078 Sequence 2 71.5 11.3 13.6 16 US-10-437-963-18308 Sequence 2 71.5 11.3 13.6 16 US-10-437-963-183078 Sequence 2 71.5 11.3 13.6 16 US-10-437-963-18308 Sequence 1 11.2 16.6 14 US-10-437-963-18308 Sequence 2 71.5 11.3 13.6 15 US-10-437-963-18308 Sequence 2 71.5 11.3 13.6 16 US-10-437-963-18308 Sequence 2 71.5 11.3 13.6 16 US-10-437-963-18308 Sequence 3 71 11.2 16.6 14 US-10-156-761-10938 Sequence 2 71.5 11.3 13.6 15 US-10-126-392-13854 Sequence 3 71 11.2 793 14 US-10-126-392-13854 Sequence 3 70.5 11.2 793 14 US-10-424-599-231854 Sequence 4 70.5 11.2 2915 13 US-10-425-114-42547 Sequence 2 70.5 11.2 2915 13 US-10-437-963-156444 Sequence 3 70.5 11.2 2915 13 US-10-437-963-156444 Sequence 1 70 11.1 123 16 US-10-437-963-153570 Sequence 1 70 11.1 123 16 US-10-437-963-153570 Sequence 2 70 11.1 123 16 US-10-437-963-153570 Sequence 2 70 11.1 1379 14 US-10-437-963-153570 Sequence 2 70 11.1 1379 14 US-10-437-963-153570 Sequence 3 70 11.1 1379 14 US-10-437-963-153570 Sequence 2 70 11.1 1379 14 US-10-437-963-153570 Sequence 3 70 11.1 1379 14	76.5 12.1 22.5 16 US-10-437-963-147024 Sequence 1 76.5 12.1 2246 16 US-10-437-963-144016 Sequence 1 76.5 12.1 2246 16 US-10-425-114-64460 Sequence 1 76.5 12.0 331 12 US-10-425-114-64460 Sequence 2 75.5 11.9 622 15 US-10-108-260A-2701 Sequence 2 75.5 11.9 701 15 US-10-108-260A-2701 Sequence 2 76.5 11.5 40.0 15 US-10-437-963-149016 Sequence 2 77.5 11.5 440 15 US-10-437-963-149016 Sequence 2 77.5 11.4 25.9 12 US-10-425-114-70983 Sequence 2 77.5 11.4 126 16 US-10-425-114-70983 Sequence 2 77.5 11.4 1126 16 US-10-425-114-40428 Sequence 2 77.5 11.3 195.1 14 US-10-029-386-32263 Sequence 2 77.5 11.3 19.6 US-10-437-963-115864 Sequence 3 77.5 11.2 14.6 14 US-10-263-929-10.5 Sequence 2 77.5 11.2 14.0 12 US-10-263-929-10.5 Sequence 3 77.5 11.2 14.0 12 US-10-263-929-10.5 Sequence 3 77.5 11.2 248 12 US-10-263-929-10.5 Sequence 3 11.2 248 12 US-10-424-599-23154 Sequence 3 11.2 248 12 US-10-424-599-23154 Sequence 3 11.2 248 12 US-10-423-963-15844 Sequence 2 70.5 11.2 248 12 US-10-423-963-15844 Sequence 3 11.2 17.3 16 US-10-437-963-15844 Sequence 2 70.5 11.2 248 12 US-10-423-963-15844 Sequence 3 11.2 17.3 16 US-10-437-963-15844 Sequence 2 11.1 12.3 13.6 US-10-437-963-15844 Sequence 3 11.1 12.3 13.6 US-10-437-963-15844 Sequence 2 11.1 12.3 13.6 US-10-437-963-15844 Sequence 3 11.1 12.3 13.6 US-10-437-963-15846 Sequence 3 11.1 13.1 14.1 12 US-10-437-963-15846 Sequence 1 11.1 13.1 14.1 15.0 US-10-437-963-15846 Sequence 1 11.1 13.1 14.1 15.0 US-10-437-963-15864 Sequence 2 11.1 13.1 13.1 13.1 13.1 US-10-437-963-15846 Sequence 3 11.1 13.1 13.1 13.1 13.1 US-10-437-963-15846 Sequence 3 11.1 13.1 13.1 13.1 13.1 13.1 US-10-437-963-15846 Sequence 1 13.1 13.1 13.1 13.1 13.1 US-10-437-963-15854 Sequence 1 13.1 13.1 13.1 13.1 13.1 US-10-437-963-15854 Sequence 2 13.1 US-10-437-963-15854 Sequence 3 13.1 US-10-437-963-15854 Sequence 3 13.1 US-10-437-963-15854 Sequence 3 13.1 US-10-437-963-15854 Sequence 3 13	5 12.6 286 16 US-10-437-963-187696 Sequence 1 5 12.1 2256 16 US-10-437-963-187696 Sequence 2 5 12.1 2246 16 US-10-437-963-164016 Sequence 2 6 12.0 331 12 US-10-245-114-64460 Sequence 2 7 12.0 331 12 US-10-245-1133 Sequence 2 15 11.9 622 15 US-10-108-260A-2701 Sequence 2 15 11.9 701 15 US-10-108-260A-2701 Sequence 2 15 11.5 137 16 US-10-437-963-149016 Sequence 2 15 11.5 137 15 US-10-399-493-18063 Sequence 3 11.5 13.1 125 14 US-10-437-963-183078 Sequence 2 15 11.4 12.5 16 US-10-425-114-70983 Sequence 3 11.4 12.5 16 US-10-425-114-40428 Sequence 3 11.4 12.5 16 US-10-425-114-40428 Sequence 3 11.3 19.5 16 US-10-425-114-40428 Sequence 2 11.3 19.5 16 US-10-425-114-40428 Sequence 3 11.3 19.5 16 US-10-425-114-40428 Sequence 1 11.3 19.5 16 US-10-425-114-40428 Sequence 2 11.3 19.5 16 US-10-425-114-40428 Sequence 2 11.3 19.5 16 US-10-437-963-115864 Sequence 2 11.3 19.5 12 US-10-29-386-32918 Sequence 3 11.2 14.0 12 US-10-29-386-32918 Sequence 3 11.2 14.0 12 US-10-29-386-32918 Sequence 3 11.2 14.0 12 US-10-424-599-231854 Sequence 4 11.2 12.3 16 US-10-425-114-42547 Sequence 1 11.1 12.3 16 US-10-437-963-115644 Sequence 1 11.1 12.3 16 US-10-437-963-115644 Sequence 1 11.1 12.3 16 US-10-437-963-15644 Sequence 1 11.1 12.3 16 US-10-437-963-15644 Sequence 1 11.1 12.3 16 US-10-425-194-164 Sequence 1 11.1 12.3 16 US-10-437-963-15644 Sequence 1 11.1 12

ALIGNMENTS

RESULT 1
US-10-001-885-125
; Sequence 125, Application US/10001885
; Publication No. US20040058319A1

GENERAL INFORMATION:

APPLICANT: Salceda, Susana
APPLICANT: Salceda, Roberto
APPLICANT: Macina, Robert
APPLICANT: Mecipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
FILE REFERENCE: DEX-0279
CURRENT APPLICATION NUMBER: US/10/001,885
CURRENT APPLICATION NUMBER: 00/252,061
PRIOR APPLICATION NUMBER: 60/252,061
PRIOR APPLICATION NUMBER: 60/253,257
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 167
SEQ ID NO 125
LENGTH: 121
TYPE: PRT
CORGANISM: Homo sapien
US-10-001-885-125 S 맑 Ś Query Match 100.0%; Score 632; DB 12; Best Local Similarity 100.0%; Pred. No. 2.4e-58; Matches 121; Conservative 0; Mismatches 0; 61 QSPFNDLNRQLVNNGFPQWHLGNHAVEPVTSILLLFLLMMLGVRGLLLLVGLVYLVSHLSQ 120 1 MVRILANGEIVQDDDPRVRTTTQPPRGSIPRQSFFNRGHGAPPGGPGPRQQQAGARLGAA 60 1 MVRILANGEIVQDDDPRVRTTTQPPRGSIPRQSFFNRGHGAPPGGPGPRQQQAGARLGAA Indels Length 121; 0; Gaps 60 Pro

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R 121

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APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghina
TITLE OP INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and I
FILE REFERENCE: DEX-0315
CURRENT APPLICATION NUMBER: US/10/076,747
CURRENT PILLING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/268,290
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: 60/268,834
PRIOR APPLICATION NUMBER: 60/268,834
PRIOR PILING DATE: 2001-02-15
SEQ ID NO 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 122
LENGTH: 121
TYPE: PAT
ORGANISM: Homo sapien
US-10-076-747-122
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US-10-076-747-122
; Sequence 122, Application US/10076747
; Publication No. US20030180726A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
APPLICANT: Karra, Kalpana
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US-09-809-391-673
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Best Local S
Matches 121
                                                                                                                                                                                                                   Sequence 673, Application US/09809391
publication No. US20030049618A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
                                                                                                                    Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 673 LENGTH: 111
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                           TYPE: PRT ORGANISM: Homo sapiens -09-809-391-673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 121; Conserv
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61 QSPENDLNRQLVNMGFPQWHLGNHAVBPVTSILLLFLLMMLGVRGLLLVGLVYLVSHLSQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Karra, Kalpana
Cafferkey, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 632; DB 14;
ilarity 100.0%; Pred. No. 2.4e-58;
Conservative 0; Mismatches 0;
  61.2%; Score 387; DB 10; 100.0%; Pred. No. 1e-32;
                        Length 111;
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PRIOR APPLICATION NUMBER: 60/047,500
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,587 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/
FILING DATE: 1997-05-23

60/047,500

APPLICATION NUMBER: 60/047,584 APPLICATION NUMBER: 60/047,581 FILING DATE: 1997-05-23

FILING DATE: 1997-05-23

APPLICATION NUMBER: 60/047,492

FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592
FILING DATE: 1997-05-23

APPLICATION NUMBER: 60/047,503 FILING DATE: 1997-05-23

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APPLICATION INVESTIGATION: IBGE Human Secreted proteins TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: PZ002P2

CURRENT APPLICATION NUMBER: U9/09/882,171

CURRENT FILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: 09/149,476

PRIOR APPLICATION NUMBER: 09/149,476

PRIOR APPLICATION NUMBER: 00/149,476

PRIOR PILING DATE: 1998-03-06

PRIOR PILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,162

PRIOR PILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,333

PRIOR FILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,626

PRIOR PILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,626

PRIOR PILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,334

PRIOR APPLICATION NUMBER: 60/040,334

PRIOR APPLICATION NUMBER: 60/040,336

PRIOR PILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,336

PRIOR APPLICATION NUMBER: 60/047,600

PRIOR PILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,615

PRIOR PILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,597

PRIOR APPLICATION NUMBER: 60/047,597

PRIOR APPLICATION NUMBER: 60/047,593

PRIOR APPLICATION NUMBER: 60/047,613

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US-09-882-171-673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 673, Application US/09882171 Publication No. US20030175858A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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OR FILING DATE: 1997-04-11
OR APPLICATION NUMBER: 60/043,672
OR FILING DATE: 1997-04-11
OR APPLICATION NUMBER: 60/043,315
OR FILING DATE: 1997-04-11
OR APPLICATION NUMBER: 60/048,974
OR FILING DATE: 1997-06-06
OR APPLICATION NUMBER: 60/056,886
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,889
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,893
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,630
OR APPLICATION NUMBER: 60/056,630
OR APPLICATION NUMBER: 60/056,630
OR APPLICATION NUMBER: 60/056,630
OR APPLICATION NUMBER: 60/056,637
OR APPLICATION NUMBER: 60/056,872
OR APPLICATION NUMBER: 60/056,873
                 OR APPLICATION NUMBER: 60/056,880
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,894
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,911
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,636
OR APPLICATION NUMBER: 60/056,636
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,874
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OR FILING DATE: 1997-04-11
OR APPLICATION NUMBER: 60/043,674
OR FILING DATE: 1997-04-11
OR APPLICATION NUMBER: 60/043,669
OR FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,568
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/043,314
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,569
FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
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                                                                    Query Match
Best Local S
Matches 73
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OR FILLING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,664
OR FILLING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,876
OR FILLING DATE: 1997-08-22
OR FILLING DATE: 1997-08-22
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OR APPLICATION NUMBER: 60/047,593

OR FILING DATE: 1997-05-23

OR APPLICATION NUMBER: 60/047,614

OR FILING DATE: 1997-05-23

OR APPLICATION NUMBER: 60/043,578
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R APPLICATION NUMBER: 60/047,586

DR FILING DATE: 1997-05-23

PR APPLICATION NUMBER: 60/047,590

DR FILING DATE: 1997-05-23

DR APPLICATION NUMBER: 60/047,594

DR APPLICATION NUMBER: 60/047,594

DR FILING DATE: 1997-05-23
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R APPLICATION
R FILING DATE:
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APPLICATION NUMBER: 60/057,650
FILING DATE: 1997-09-05
APPLICATION NUMBER: 60/056,884
                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1997-08
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,909
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,670
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/056,875
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APPLICATION NUMBER: 60/043,576
FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-
APPLICATION NUMBER: 6
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APPLICATION NUMBER: 60/
FILING DATE: 1997-05-23
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,631
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,761
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APPLICATION NUMBER: 6
FILING DATE: 1997-08-
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                                                                                                   Similarity
                      MVRILANGEIVQDDDPRVRTTTQPPRGSIPRQSFFNRGHGAPPGGPGPRQQQAGARLGAA
                                                                                                                                                                                  DATE: 1997-09-05
                                                                 61.2%; Scilarity 100.0%; F
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E: 1997-04-11
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NUMBER: 60/
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                                                                                             Score 387; DB 10;
Pred. No. 1e-32;
                                                                         Mismatches
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60 0 FILING DATE:

1997-04-

FILING DATE: APPLICATION NUMBER:

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DATE: 1997-05-

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APPLICANT: Rosen et al.
APPLICANT: ROSEN et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-03-06
NUMBER: OF ZGO ID NOS: 757
NUMBER OF ZGO ID NOS: 757
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US-09-809-391-367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-861-673
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Publication No. US20030049618A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
                                                                                                                                                                                                                                                                                                                                                       Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 367
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ORGANISM: Homo sapiens
-09-809-391-367
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CURRENT FILING DATE: 2001-03-16
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o. US20030225248A1
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                                                                                                                                                           Conservative
                                                                                                                                                           38.8%; Score 245; DB 10; 100.0%; Pred. No. 2.9e-18; tive 0; Mismatches 0;
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PRIOR FILING DATE: 1998-03-06
PRIOR PRIOR APPLICATION NUMBER: 60/040,162
PRIOR PRILING DATE: 1997-03-07
PRIOR PILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,626
PRIOR PILING DATE: 1997-03-07
PRIOR PILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,334
PRIOR PILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,334
PRIOR PILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,336
PRIOR PILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,336
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PRIOR FILING DATE: 1997-03-07
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PRIOR FILING DATE: 1997-05-23
PRIOR PELICATION NUMBER: 60/047,618
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,503
PRIOR APPLICATION NUMBER: 60/047,592
PRIOR APPLICATION NUMBER: 60/047,592
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Publication No. US20030175858A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-06-18
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PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,615
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,597
PRIOR FILING DATE: 1997-05-23
PRIOR FILING DATE: 1997-05-23
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PRIOR APPLICATION NUMBER: 60/047,582
PRIOR FILING DATE: 1997-05-23
PRIOR FILING DATE: 1997-05-60/047,596
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PRIOR APPLICATION NUMBER: 60/047,613
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,601
FILING DATE: 1997-05-23
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                                                                 APPLICATION NUMBER: 60/047,632
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APPLICATION NUMBER: 60/047,612
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APPLICATION NUMBER: 60/047,500
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                                                                                              1997-05-23
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OR APPLICATION NUMBER: 60/056,888
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,879
OR APPLICATION NUMBER: 60/056,880
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,894
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,911
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,911
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,636
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,874
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,910
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,631
OR APPLICATION NUMBER: 60/056,845
OR APPLICATION NUMBER: 60/056,845
OR APPLICATION NUMBER: 60/056,845
OR APPLICATION NUMBER: 60/056,892
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OR APPLICATION NUMBER: 60/043,311
OR APPLICATION NUMBER: 60/043,671
OR APPLICATION NUMBER: 60/043,671
OR APPLICATION NUMBER: 60/043,674
OR APPLICATION NUMBER: 60/043,674
OR APPLICATION NUMBER: 60/043,312
OR APPLICATION NUMBER: 60/043,313
OR APPLICATION NUMBER: 60/043,315
OR APPLICATION NUMBER: 60/048,974
OR APPLICATION NUMBER: 60/056,886
OR FILING DATE: 1997-04-11
OR APPLICATION NUMBER: 60/056,886
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,893
OR APPLICATION NUMBER: 60/056,630
OR APPLICATION NUMBER: 60/056,632
OR APPLICATION NUMBER: 60/056,633
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US-10-164-861-367
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    Sequence 367, Application US/10164861
publication No. US20030225248A1
GENERRAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: E2002P1
CURRENT APPLICATION NUMBER: US/10/164,861
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Best Local S
Matches 48
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OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,614
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/043,578
OR APPLICATION NUMBER: 60/043,578
OR PILING DATE: 1997-04-11
OR PILING DATE: 1997-04-11
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,501
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/056,632
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,632
OR APPLICATION NUMBER: 60/056,632
OR APPLICATION NUMBER: 60/056,632
OR APPLICATION NUMBER: 60/056,876
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: 60/056,881
OR APPLICATION NUMBER: 60/056,881
OR APPLICATION NUMBER: 60/056,909
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OR APPLICATION NUMBER: 60/048,964
OR FILING DATE: 1997-06-06
OR APPLICATION NUMBER: 60/057,650
OR FILING DATE: 1997-09-05
OR APPLICATION NUMBER: 60/056,884
OR APPLICATION NUMBER: 60/057,669
OR APPLICATION NUMBER: 60/057,669
OR FILING DATE: 1997-09-05
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R FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,594
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,589
OR APPLICATION NUMBER: 60/047,589
OR FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,599
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,585
FILING DATE: 1997-05-23
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; Pred. No. 2.9e-18;
0; Mismatches 0;
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PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR

APPLICATION NUMBER: 60/043,569 FILING DATE: 1997-04-11

FILING DATE: 1997-04-

FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,568
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,314

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Length Indels

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Gaps

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CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR APPLICATION NUMBER: DS/09/149,476
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 367
LENGTH: 48
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US-10-156-761-10980
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APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAHBA, TADAYOSHI
APPLICANT: SAHAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
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US-10-164-861-367
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TITLE OF INVENTION: No. US20040005560A1el full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3882, Application US/10108260A Publication No. US20040005560A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                     93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 GNHAVEPVISILLLFLLMMLGVRGLLLVGLVYLV 115
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US-10-437-963-198292
; Sequence 198292, Application US/10437963
; Publication No. US20040123343A1
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SEQ ID NO 10980
LENGTH: 223
                                                                                                APPLICANT:
APPLICANT:
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Best Local Similarity
Matches 29; Conserva
                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                            APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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Local Similarity 32.8%;
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                                                                                                               Cao, wei
                                                                                                                                      Zhou, Yihua
Cao, Yongwei
                                                                                                Boukharov, Andrey A.
                                                          Li, Ping
                                                                             Barbazuk, Brad
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CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 174474
LENGTH: 112
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APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_128569C.1.pep
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                                                   37 RGHGAPPGGPGPRQQQAG-ARLGAAQSPFND------LNRQLVNMGPPQWHLGNHA 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 VNMGFPQWHLGNHAVEPVTSILLLFLLMMLGVRG 105
RGEGSPPPGKGPRSGAAGKGRAGGAKPPPNPLLVPFAGVILLNKEQPVFALARWKIPVSK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPPYPQAPGGIPQQGYGYPQQGQPGYGYPGGPGGPGPRVASMGRRLGA----
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                                                                                                            Score 85.5; DB 12; Length 112; Pred. No. 0.4; 8; Mismatches 26; Indels 11
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RESULT 14
US-10-106-698-8371
; Sequence 8371, Application US/10106698
; Publication No. US20030109690A1
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US-10-425-114-60982
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US-10-437-963-198292
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-425-114-60982
GENERAL INFORMATION:
APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PC7/US00/26524
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 60982
LENGTH: 256
TYPE: PRT
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NUMBER OF SEQ ID NOS:
SEQ ID NO 198292
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Zea mays
FEATURE:
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ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                            70
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29; Conservative
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Similarity 42.9%;
27; Conservative
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Screen, Steven E
Tabaska, Jack E
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Pred. No. 3.1;
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Pred. No.
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                                                                                                 ; ORGANISM: Streptomyces avermitilis US-10-156-761-10160
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                                   Query Match
Best Local S
Matches 37
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PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTMARE: Patentin Ver. 3.0
SEQ ID NO 8371
                                                                                                                                               NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10160
LENGTH: 392
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10160, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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Best Local
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APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
                                                                                                                                                                                           PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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NAME/KEY: MISC_FEATURE
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NAME/KEY: MISC_FEATURE
LOCATION: (6)
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NAME/KEY: MISC_FEATURE
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NAME/KEY: MISC_FEATURE
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                                 1 Similarity 37; Conserv
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HORIKAWA, HIROSHI
                                   Conservative
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   ---TTQPPRGSIPRQSFFNRGHG---
                                 Score 80; DB:
Pred. No. 6.6;
18; Mismatches
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Sear Job	Дb	γQ	B	Ş	ф
Search completed: August 24, 2004, 09:33:21 Job time : 126 secs	160 AVVVGLWELTSRLEER 175	107 -LLVGLVYLVSHLSQR 121	120 QKKSAGRDLGAAIGVGVGLGVVIVASLEVVKAVEVGVIAV 159	49 RQQQAGARLGAAQSPENDLNRQLVNMGFPQWHLGNHAVEEVTSILLLFLLMMLGVRGL 106	67 SGPLFRDDTPQTTSYGSQTPYVTQSPYGSQTPHGAQPQKPEPMPDAPQPAPAP 119

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US.10001885/runat_17082004_151718_25904/app_query.fasta_1.263
-Q=/cgn2_1/USPTO_spool_p/US.10001885/runat_17082004_151718_25904/app_query.fasta_1.263
-DB-GenEmbl -QPWT_fastap_SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTEMT=pco -NOME=sext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10001885_@CGN 1 1_5600_@runat 17082004 151718_25904 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAXLT -DSPBLCCK=100 -LONGING
-DEV_TIMEOUT=120 -MAXN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEVEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
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-MODEL=frame+_p2n.model -
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Perfect score:
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Ygapop 10.0 , X
Fgapop 6.0 , E
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                                                               US-10-001-885-125
632
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29: em vi:*
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40: em htg_orber:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

RESULT

ALIGNMENTS

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Percent Similarity:
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AUTHORS
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1 (bases 1 to 1049)

RS Ruben, S.M., Rosen, C.A., Fischer, C.L., Soppet, D.R., Carter, K.C., Bednarik, D.P., Endress, G.A., Yu, G.L., N.J., Feng, P., Young, P.E., Greene, J.M., Ferrie, A.M., Duan, R., Hu, J.S., Florence, K.A., Olsen, H.S., Ebner, R., Brewer, L.A., Moore, P.A., Shi, Y., Lafleur, D.W., Li, Y., Zeng, Z. and Kyaw, H.

186 human secreted proteins
Patent: JP 2002510192-A 57 02-APR-2002;
HUMAN GENOME SCIENCES INC
PN JP 2002510192-A/57
PD 02-APR-2002
PN JP 2002510192-A/57
PD 02-APR-1997 US 60/040162,07-MAR-1997 US 60/04033 PR
07-MAR-1997 US 60/040162,07-MAR-1997 US 60/040161 PR
07-MAR-1997 US 60/04036,07-MAR-1997 US 60/04033 PR
07-MAR-1997 US 60/04036,07-MAR-1997 US 60/04036 PR
07-MAR-1997 US 60/04036,07-MAR-1997 US 60/040163 PR
07-MAR-1997 US 60/04058,07-MAR-1997 US 60/040163 PR
07-MAR-1997 US 60/04058,07-MAR-1997 US 60/040163 PR
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07-MAR-1997 US 60/04058 PR
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JP 2002510192-A/57.
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186 human secreted proteins.
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            C12N15/12,C12N5/10,C12N1/21,C07K14/47,C07K16/18,C12Q1/68, PC
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/mol_type="genomic DNA"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(CS 1 (bases 1 to 1129)

Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J.G.,
Klausner, R. D., Collins, F.S., Wagner, L., Shenmen, C. M., Schuler, G. D.,
Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Histeh, F.,
Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,
McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. M.,
Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,
Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,
Fahey, J., Helton, E., Ketteman, M., Wadan, A., Kodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,
Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,
Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Wyers, R. M.,
Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E.,
Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

P. Dickson, M. C., Schein, J. E., Jones, S. J. and Marra, M. A.

Generation and mouse cDNA sequences

P. Dickson, M. C., Schein, J. E., Jones, S. J. and Marra, M. A.

Generation and mouse cDNA sequences
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                                                                                        NTH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC013587 1129 bp mRNA lin
Homo sapiens chromosome 10 open reading frame
MGC:9596 IMAGE:3896656), complete cds.
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Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Clone distribution: MGC clone distribution information can be found through the I M A.G E Consortium/LLNL at: http://image.llnl.gov
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This clone was selected for full length sequencing because it

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ource DS	1.64e-43 Length: 632.00 Matches: 100.00\$ Conservative: 100.00\$ Mismatches: 100.00\$ Indels: 9 Gaps:	Alignment Scores: Pred. No.: Score: Percent Similarity Best Local Similar Query Match: DB:
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rce 1. 1129 1. 1129 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="MGC:9596 IMAGB:3896656" /tissue_type="Pancreas, epithelioid carcinoma/clone_Tib="NIH_MGC_70" /lab_host="UH10B" /note="Vector: pCMV-SPORT6" 1. 1129 e /gene="C10orf35"	ocusID:21973	CDS
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                                                                                                               Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Harlocker,S.L., Dillon,D.C. and Xu,J.

Dna sequences from breast tumor and uses thereof
Patent: WO 0127276-A 5 19-APR-2001;

CORIXA CORPORATION (US)

Location/Qualifiers

1. .550
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Sequence 5 from Patent WO0127276.
AX113082 GI:13939514
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
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1. .1192
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/mol_type="unassigned DNA"
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RESULT 5
BC024943
LOCUS
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSIÓN
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-001-885-125 (1-121) x AX113082 (1-550)
                                                                                                                                                                                                                                                                                                                                                         REFERENCE
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                                                                                                                                                                                                                                                                                                                                       AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 22 1 (bases 1 to 1538)

El (bases 1 to 1538)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altechul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Cassavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Wollalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Boutfard G G Blakesley,R M, Touchman,J W, Green,B D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 ATGGTGCGGATCTTGGCCAATGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC024943

1538 bp mRNA linear ROD 06-OCT-2003

Mus musculus RIKEN cDNA 2010107G23 gene, mRNA (cDNA clone MGC:28201

IMAGE:3989515), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC024943.1 GI:19354288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC024943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTACCCAGCCAACAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCCATGGT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tLeuGlyValArgGlyLeuLeuLeuValGlyLeuValTyrLeuValSerHisLeuSerGl 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuGlyAsnHisAla-ValGluProValThrSerIleLeuLeuLeuPheLeuLeuMetMe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGTCCCCTTCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCAT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCGGCAACCATGCTTGTGGAGCCGGTGACCTCCATCCTGCT-CTCCTTCCTGCTCATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="unassigned DNA"
/db_xref="taxon:9606"
1. .550
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577.00
97.52%
96.69%
91.30%
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COMMENT
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MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
  US-10-001-885-125 (1-121) x BC024943 (1-1538)
                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 36 Row: h Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 1538)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="MGC:28201 IMAGE:3989515"
/tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV."
/clone lib="NCI CGAP_Lu29"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .1538
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PGBRQQDAGARCGAAQSPS
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                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1/product="2010107G23Rik protein"/product="2010107G23Rik protein"/protein id="AAH24943.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="2010107G23Rik"
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/db_xref="MGI:1917144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:10090"
                                                    4.08e-38
568.50
94.21%
92.56%
89.95%
                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                       1538
112
6
1
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS RESULT 6 AC116233/c DEFINITION RS Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Asguliano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Ballerin, D., Bandaranaike, D., Barber, M., Barastead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Crockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dumn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagge, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregoorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W., Harvey, Y., Hawlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Hernandez, J., Howells, S., Hilyk, S., Hune, J., Idebird, D., Jackson, A., Levan, J., Lewis, L., Li, Z., Liu, J., Loudeged, H., Lovan, J., Lewis, L., Li, Z., Liu, J., Maheshwari, M., Mahindarthe, M., Mahnoud, M., Malloy, K., Mangum, A., Mandun, P., Martin, R., Mortenayor, J., Moore, S., Mollos, S., Munidasa, M., Murphy, M., Nair, L., Mangum, A., Martin, S., Montemayor, J., More, S., Mollos, S., Munidasa, M., Murphy, M., Nair, L., Mangum, N., Nai 843 121 783 101 663 603 546 ACCACCCAG---CACAGAAGTAGTAGCTCTCAGCAGGGCTTTTTCAACAGAGGCCACGGC 723 486 81 61 41 21 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Veri AC116233 275924 bp DNA linear Rattus norvegicus clone CH230-95L17, *** SEQUENCING AC116233.7 GI:23101097 Arg CTCGGGGTTCGTGGCCTCCTGCTTGTGGGCCTGGTCTACCTGACTCAGCTCAG LeuGlyValArgGlyLeuLeuValGlyLeuValTyrLeuValSerHisLeuSerGln 120 င္ပရ GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis AlaProProGlyGlyProGlyProArgGlnGlnGlnAlaGlyAlaArgLeuGlyAlaAla LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuLeuMetMet CTTGGGAACCACGTGGGAACCTGTGACCTCCATCCTCCTGCTCTTCCTGCTTATGATG CAATCTCCTTTCAGTGACCTGAACCGGCAGCTGGTGAACATGGGCTTCCCACAATGGCAC ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGly MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspAspProArgValArgThr (bases 1 to 275924) 845 121 unordered pieces. Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; HTG 22-SEP-2002 IN PROGRESS 842 100 722 60 40 545 20 782 80 662 602

> TITLE
> JOURNAL
> REFERENCE
> AUTHORS
> TITLE
> JOURNAL REFERENCE AUTHORS TITLE JOURNAL Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzzo, M., Quircz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodeggren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wallson, R., Walers, R., Wei, X., White, F., Williams, G., Willson, R., Walers, R., Wei, X., White, F., Williams, G., Willson, R., Walers, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Zhou, X., Zhao, S., Dunn, D., von, V., Yu, F., Zhang, J., Zhou, X., Zhou, S., Dunn, D., von, V., Weinstock, G. and Gibbs, R.A. Submitted (22-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
> On Sep 18, 2002 this sequence version replaced gi:21738715.
> The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/fat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table. Submitted (26-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 275924)
> Rat Genome Sequencing Consortium. Worley, K.C. Direct Submission Direct Submission Unpublished 2 (bases 1 to 275 Nwaokelemeh,O., Direct Submission (bases 1 to 275924) Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Department

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COMMENT

Center project name: GRFW
Center clone name: CH230-95117
Center clone name: CH230-95117
Center clone name: CH230-95117
Assembly program: Phrap; version 0.990329
Consensus quality: 234606 bases at least Q40
Consensus quality: 23765 bases at least Q20
Consensus quality: 238894 bases at least Q20
Estimated insert size: 264374; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ ----- Genome Center

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a "working draft' sequence. It currently
consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved. 10839 10939 273286 273386 274619 10838: contig of 10838 bp in lengt:
10938: gap of unknown length
273285: contig of 262347 bp in leng:
273385: gap of unknown length
274618: contig of 1233 bp in length
274718: gap of unknown length in length

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RESULT 7
AR413227
LOCUS
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Best Local Similarity:
Query Match:
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                                                                                                                                             LeuGlyValArgGlyLeuLeuLeuValGlyLeuValTyrLeuValSerHisLeuSerGln 120
                                                                                                                                                                                                                                                                                                                                                                                 GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis
                                                                                                                                                                                                                           CTTGGGAACCACGTGGTGGAGCCTGTGACCTCCATCCTCCTGCTCCTGCTCATGATA
                                                                                                                                                                                                                                               LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuLeuMetMet 100
                                                                                                                                                                                                                                                                                                       CAATCTCCTTTCAGTGACCTGAACCGGCAGCTGGTGAACATGGGCTTCCCACAATGGCAT
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/note="clone_boundary
clone_end:T7
site:EcoRI
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/mol type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-95L17"
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BD108780
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Unclassified.

El (bases 1 to 483)

E dwards,J.-B.D.M., Jobert,S. and Giordano,J.

E ST's and encoded human proteins

BAL Patent: US 6639063-A 864 28-OCT-2003;

Location/Qualifiers

1. 483

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1. Teanism="unknown"
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PATENT: JP 2
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OS Homo sa:
PN JP 2002
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PD 15-JAN-
PF 07-AUG-
PR 05-AUG-
PI JEAN BA
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AR413227.1
                                                                                                                                 Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 483)

Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.

EST and encoded human protein

Fatent: JP 2002010789-A 857 15-JAN-2002;
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EST and encoded human protein.
BD108780
BD108780.1 GI:23203598
JP 2002010789-A/857.
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Homo sapiens (human)
JP 2002010789-A/857
15-JAN-2002
15-JAN-2000 JP 2000280989
05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
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483

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DNA

linear

PAT 18-DEC-2003

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Percent Similarity: Best Local Similarity: US-10-001-885-125 (1-121) x BD108780 Query Match: Alignment Scores: FEATURES source No.: PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC C12N1/21,
PC C12N15/00,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC C12N15/00
CC EST and encoded human protein FH Key Location/Qualifiers
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/db_xref="taxon:9606" 171. .4 Location/Qualifiers 3.42e-37 551.00 100.00% 100.00% 87.18% Mismatches: Indels: Length: Matches: Conservative: Gaps: 483 104 0

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(1-483)

AC111675/c LOCUS REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE S 밁 Ś 밁 Ś 片 Ş 멍 Ś 밁 멍 Ś DEFINITION ORGANISM 471 101 411 351 291 231 ACTACCCAGCCACAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGT 171 81 61 41 21 Muzny, D. Marie, M. Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, D., Anguialebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Burstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., ACI11675

240657 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus Clone CH230-48G14, WORKING DRAFT SEQUENCE, 4
unordered pieces.
ACI11675
ACI11675
ACI11675
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BC1:30579217
HTG: busco: '''''' HTG; HTGS_PHASE1; HTGS_DRAFT; Rattus norvegicus (Norway rat) Rattus norvegicus Bukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Rattus AlaProProGlyGlyProGlyProArgGlnGlnGlnAlaGlyAlaArgLeuGlyAlaAla LeuGlyValArg 104 CTTGGTGTTCGT LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuLeuMetMet CAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCAT GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGly MetValArgI1eLeuAlaAsnGlyGluI1eValGlnAspAspAspProArgValArgThr (bases 1 to 240657) 482 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; HTGS_FULLTOP , Dederich, D., , Divya, K., 230 470 100 410 60 40 80 350 290 20

> Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eayes, K., Eggan, A., Escotto, M., Eugens, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flaggy, T., Forbes, L., Foster, M., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guerra, W., Handland, W., Hamil, C., Hamilton, C., Hamilton, K., Hernandez, J., Hines, S., Hladann, S.L., Hodgson, A., Hogues, M., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hernandez, J., Jackson, A., Jackson, J., Longacre, S., Lopez, J., Liu, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R., J., Lu, X., Ma, J., Liu, X., Kally, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Martin, R., Martin, R., Martinez, B., Montensayor, J., Moore, S., Lopez, J., Loussey, J., London, P., Longacre, S., Lopez, J., Loussey, J., Loussey, J., Loussey, J., London, P., London, P., Longacre, S., Lopez, J., Mandhiney, S., McLeod, M., Mahnoud, M., Mahloy, K., Mangum, A., Mahnoud, M., Mahloy, K., Mangum, A., Martin, R., Ma Submitted (13.MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
> On May 13, 2003 this sequence version replaced gi:24818892.
> The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome Submitted (19-FEB-2002) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 240657) Rat Genome Sequencing Consortium. shotgun sequence table. Direct Submission Worley, K.C. Direct Submission Unpublished Direct Submission (bases 1 to 240657)

REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

----- Genome College Center llege of Medicine

Contact: hgsc-help@bcm.tmc.edu Web site: http://www.hgsc.bcm.tmc.edu/ Center: Baylor Co

Center project name: GMVI Center clone name: CH230-48G14

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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                    ACCACCCAA---CAGAGGAGTAGCAGCACCCGGCAGGGCTTTTTCAACAGAGGCCACAGT 51506
                                                                                                                                                                          MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspAspProArgValArgThr 20
                                                                                                                ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGly 40
AlaProProGlyGlyPro-GlyProArgGlnGlnGlnAlaGlyAlaArgLeuGlyAlaAl 60
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Consensus quality: 228778 bases at least Q40
Consensus quality: 231963 bases at least Q30
Consensus quality: 231939 bases at least Q20
Estimated insert size: 237555; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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/note="wgs end extension clone end:Sp6"
8292. ...9121
/note="clone boundary clone end:Sp6"
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complement(233966...234793)
/note="clone_boundary
clone_end:T7
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243065" Rattus norvegicus"
/mol_type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-48G14"
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236911: gap of unknown length
238255: contig of 1344 bp in length
238355: gap of unknown length
238355: contig of 1150 bp in length
239505: gap of unknown length
239605: gap of unknown length
240657: contig of 1052 bp in length
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  RESULT 11
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US-10-001-885-125 (1-121) x AR415427 (1-519)
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Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 3064 28-OCT-2003;
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Sequence 3064 from patent
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/mol_type="genomic DNA"
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C12N1/21,
PC C12N15/00
CC EST;
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Edwards, J. B.D.M., Jobert, S. and Giordano, EST and encoded human protein
Patent: JP 2002010789-A 3057 15-JAN-2002;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                             Homo sapiens
                                            Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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15-JAN-2002
07-AUG-2000 JP 2000280989
05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN
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                                                                                                                       165110 bp DNA ]
sequence from clone RP11-343J3 on
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORKVEEP; Information on the WORKVEEP database can be found at primary accession on the WORKVEEP database can be found at part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 http://www.sanger.ac.uk/Profects/Crelo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (12-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 8, 2001 this sequence version replaced gi:14575291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/HGP/Chr10
RP11-343J3 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is the entire insert of clone RP11-34303 The true left.end of clone RP11-242620 is at 139955 in this sequence. The true right end of clone RP11-404C6 is at 6588 in this sequence. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSx repeat: matches 118. 5662. .6438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluSg repeat: matches 1. .310 of consensus"
4144. .4270
/note="AluSx repeat: matches 1. .134 of consensus"
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                                                           13433.
                                                                                                             /note="20 copies
L2479. .12608
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/note="MIR repeat:
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2960. .3272
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                   'note="65 copies 2
                                                                                                                                                                                                 note="AluSx repeat: matches 1. .294 of consensus"
                                                                                                                                                                                                                                                      'note="MIR repeat: matches 65. .194 of consensus"
                                                                                                                                                                                                                                                                                                                                                                 note="LIMEc repeat: matches 1168. .2367 of consensus"
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                                                                                                                                                                      .11639
                                                              .13876
                             repeat: matches
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                                                                                   mer at 90% conserved"
                                                                                                                                                                                                                                                                                                               matches 25. .184 of consensus"
                                                                                                                                           mer
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23388. .2353
/note="L2 repeat: matches 2097. .2230 of consensus"
23533. .23837
/note="AluJb repeat: matches 1. .303 of consensus"
23838. .248137
/note="MIR repeat: matches 1754. .2097 of consensus"
24291. .24581
/note="MIR repeat: matches 1. .300 of consensus"
/note="MIR repeat: matches 1. .300 of consensus"
/note="MIR repeat: matches 1. .200 of consensus"
24653. .24850
/note="MIR repeat: matches 1. .200 of consensus"
26189. .26685
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14577..14633
/note="hluSq repeat: matches 243..299 of consensus
14843..14943
/note="MER86 repeat: matches 9..109 of consensus"
/note="MER86 repeat: matches 9..109 of consensus"
/note="MIR repeat: matches 3..213 of consensus"
/note="MIR repeat: matches 60..140 of consensus"
/note="MIR repeat: matches 60..140 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MLTIJU repeat: matches 1..62 of consensus"
/20889. .21263
/note="MLTIF repeat: matches 188. .541 of consensus"
21463. .21618
/note="MLR repeat: matches 46. .192 of consensus"
/note="MLR repeat: matches 46. .192 of consensus"
/2019. .22366
/note="Aluub repeat: matches 1. .306 of consensus"
/22381. .22564
                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
29453..30918
/note="CpG island"
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,9969. .20010

10621 .20704

10618 - 120704 2 mer gt 85% conserved 2 more gt 85% conserved 2 more gt 85% conserved 3 more gt 85% conser
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[9169. .19400
Inote="MIR repeat: matches 5. .239 of consensus"
[9436. .19627
Inote="ILIMC5 repeat: matches 7728. .7917 of consensus"
/evidence=not_experimental
36551, .36604
                                                                                               note="AluJo repeat: matches 29.
12767. 32830
12767. 32830
13050. .33178
13050. .33178
13050. .33178
                                                                                                                                                                                                                                                         evidence=not experimental
|1084..31156
| note="MIR repeat: matches 65..138 of consensus"
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note="U2 repeat: matches 1. .36 of consensus"
0802. .20863
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note="33 copies 2 mer gg 66% conserved"
7476. .17569
                                               5112. .36201
note="CpG island"
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                                                                                                                                                                                                                                                                                                                                                                                                                     note="CpG island"
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_e="LIMC4 repeat: matches 7617. .7977 of consensus"
.7. .18345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e="L2 repeat: matches 2453. .2629 of consensus"
6. .23174
6e="MLTIJ repeat: matches 117. .413 of consensus"
5. .23346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e="MIR repeat: matches 48. .131 of consensus"
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                                                                                                          conserved"
                                                                                                                                                            .139 of consensus"
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                                                                                                                                                                       72 ValAsnMetGlyPheProGlnTrpHisLeuGlyAsnHisAlaValGluProValThrSer 91
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                                                                                                                                           GTGAACATGGGCTTTCCGCAGTGGCATCTTGGCAACCATGCTGGAGCCGGTGACCTCC
                                                             /note="LIPA15 repeat: matches 5480. .6157 of consensus"
38265. .38561
/note="Alusx repeat: matches 1. .300 of consensus"
39214. .39423
/note="MIR repeat: matches 3. .219 of consensus"
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41057. .41290
/note="MIR repeat: matches 8.
41296. .41460
/note="L2 repeat: matches 2569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluSq repeat: matches 1. .287 of consensus" 50980. .51291
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/note="23 copies 2 mer gt 97% conserved"
50684. .50969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MER58A repeat: matches 37.
45798. .45909
Moote="LTR41 repeat: matches 90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44600. .44956
/note="LTR16A repeat: matches 90.
45240. .45300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="L2 repeat: matches 1916. .2416 of consensus"
|2388. .42698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Alusx repeat: matches 1.
10050. .40189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="I1M4 repeat: matches 3652.
4648. .54862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="FAM repeat: matches 2. .167 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="LIM4 repeat: matches 3865. .4055 of consensus" 4261. .54432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Alusx repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="LTR41 repeat: matches 11.
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .217 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .365 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .97 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .445 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .3865 of
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                                            90308
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Val TyrlenVal SerHisLeuSerG

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RESULT 13

REFERENCE

KEYWORDS

VERSION ACCESSION

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AUTHORS JOURNAL

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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dodge, S., Domino, M., Doyle, M., Ferreira, P., FittHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Leboczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., Menga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Scojanovic, N., Subramanian, Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vossiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, T., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 5, 2000 this sequence version replaced gi:6984451.
All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-JAN-2000) Whitehead Institute/MIT Center for Genomers and Charles Street, Cambridge, MA 02141, USA 3 (Dases 1 to 173341)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen, Anderson,S., Baldwin,J., Barra,N., Bastien,Y., Beda,F., Boukhgalter,B., Brown,A., Burkett,G., Campophano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., DistaryJ.S., Decino, M., Cooke, P., DeArellano,K., Dewar,K., DistaryJ.S., Decino, M., Dearellano,K., Dewar,K., DistaryJ.S., Decino, M., Dearellano,K., Dewar,K., Desar,K., Desar,K.
                                                                                                                                                                                                                                                                                         All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
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HTG; HTGS_PHASE1; HTGS
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(bases 1 to 173341)
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Contact: sequence_submissions@genome.
                                                                                                                          Center code: WIBR
                                                                                                                                                                     Center: Whitehead Institute/ MIT Center
                                                                         site:
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                                                                   http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG 24-AUG-2002
WORKING DRAFT
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REFERENCE

AUTHORS

TITLE

JOURNAL

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source

JOURNAL

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Center project name: L5931

Center clone name: 57 E 12

Center clone name: 57 E 12

Center clone name: 57 E 12

Sequencing vector: M13, M77815; 100% of reads Sequencing vector: M13, M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 16190 bases at least Q40 Consensus quality: 166877 bases at least Q20 Consensus quality: 168975 bases at least Q20 Insert size: 176040; agarose-fp Theory Coverage: 3.7 in Q20 bases; agarose-fp Quality coverage: 3.8 in Q20 bases; sum-of-contistic Continuous Contraction Continuous Contraction Continuous Contraction Continuous Contraction Continuous Contraction Continuous Contraction Contract
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be preserved.
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                                128891
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147290: contig o
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Location/Qualifiers
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106598: gap of
116598: contig
117086: gap of
117086: gap of
128890: contig
128990: gap of
147290: contig

    Project Information

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f 100 bp
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                           US-10-001-885-125 (1-121) x AC021954 (1-173341)
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3144. .5889
/note="assembly_fragment"
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clone_end:SP6
vector_side:left"
27487._.32572_
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clone_end:T7
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43836. .49020
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/db_xref="taxon:9606"
/chromosome="10"
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/clone lib="RPCI-11 Human Male
1. .1574
                                                                                                                                                                                                                               /note="assembly_fragment"
147391. .173341
/note="assembly_fragment"
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|06599. .116986
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13775. .18831
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KEYWORDS
SOURCE
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                                                                                                           Sequencing vector: M13; 0%
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 212279 bases at least Q40
Consensus quality: 213137 bases at least Q30
Consensus quality: 213590 bases at least Q20
Insert size: 192000; agarose-fp
Insert size: 192000; agarose-fp
Quality coverage: 10.54 in Q20 bases; sum-of-contigs
Quality coverage: 10.54 in Q20 bases; sum-of-contigs
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AC127417
AC127417
AC127417
AC127417 2 GI:24137619
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

Mus musculus (house mouse)

Mus musculus (bouse mouse)

Mus musculus
Eukarvor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McPherson, J.D. and Waterston, R.H.

Mirect Submission
Submitted (15-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 215050)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (19-OCT-2002) Genome Sequencing Center, 4444 Forest
Farkway, St. Louis, MO 63108, USA
On Oct 19, 2002 this sequence version replaced gi:21759524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 215050)
McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing Center
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RESULT 15
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                                       DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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258815 bp DNA linear HTG 19-NOV-2002
Rattus norvegicus clone CH230-259G16, WORKING DRAFT SEQUENCE, 3
unordered pieces.
                                                                                                                                                   ValTyrLeuValSerHisLeuSerGlnArg 121
                                                                                                                                                                                                                                                                           GTGAACATGGGCTTCCCACAATGGCACCTTGGGAACCACGTGGTGGAACCTGTGACCTCC
                                                                                                                                                                                                                                                                                                                                               CAGGCAGGTGCCCGACTGGGTGCTGCCCAATCTCCTTTCAGTGACCTGAACCGGCAGCTG
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49798
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27419. .49797
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79479. .132595
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'db_xref="taxon:10090"
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.32696. .215050
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16689: gap of unknown length
27318: contig of 10629 bp in length
27418: gap of unknown length
4979: contig of 22379 bp in length
49879: contig of 22481 bp in length
49879: gap of unknown length
79378: contig of 29481 bp in length
79379: contig of 53117 bp in length
132595: contig of 53117 bp in length
132695: gap of unknown length
215690: contig of 82355 bp in length.
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                                                                                                                                                                                                                       Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 258815)
Rat Genome Sequencing Consortium.
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 19, 2002 this sequence version replaced gi:23912578. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 williams, G., willson, R., wieczyk, R., wooden, H., worley, K., wright, D., wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., weinstock, G. and Gibbs, R.A.
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HTG; PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project name: GZXS
Center project name: CH230-259G16
Center clone name: CH230-259G16
Center clone name: CH230-259G16
Consensus quality: 224747 bases at least Q40
Consensus quality: 227981 bases at least Q30
Consensus quality: 227982 bases at least Q30
Consensus quality: 227983 bases at least Q40
Consensus quality: 227983 bases at least Q40
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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0 258815: contig of 1366 bp in length.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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70.89%
    Conservative: Mismatches: Indels: Gaps:
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US-10-001-885-125 (1-121) x AC127817 (1-258815)

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112 220140	92 220200	72 220260	52 220320	32 220380
112 ValTyrLeuValSerHisLeuSerGlnArg 121 	92 IleLeuLeuLeuPheLeuLeuMetMetLeuGlyValArgGlyLeuLeuLeuValGlyLeu 111 	72 ValAsnMetGlyPheProGlnTrpHisLeuGlyAsnHisAlaValGluProValThrSer 91	52 GInAlaGlyAlaArgLeuGlyAlaAlaGlnSerProPheAsnAspLeuAsnArgGlnLeu 71	32 GlnSerPhePheAsnArgGlyHisGlyAlaProProGlyGlyProGlyProArgGlnGln 51

Search completed: August 22, 2004, 09:14:41 Job time : 2208 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

Result Score No. Score 1 632 2 632 3 632 5 632 6 632 6 632 6 632 7 6 632 7 6 632	Database : Pred. Nacore gand is	Command line parameters:	Post-processing:	Minimum DB seq Maximum DB seq	Total number	Searched:	Scoring table:	Title: Perfect score: Sequence:	Run on:	OM protein -
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	geneseq_29Jan04:* geneseqn1980s:* geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2001as:* geneseqn2003as:* geneseqn2003bs:* geneseqn2003ds:* geneseqn2003ds:* geneseqn2003ds:* geneseqn2003ds:* geneseqn2003ds:* the number of resu	nmeters: nmodel DEV=xlp spool, yUS1000188 spool, OFMT=fastap sabits -START=1 -E NMT=good -THR SCORE=; NMT=gto -NGEM=ext GCGN 1 1 708 @run GCGN -NEG SCORES=0 -WARN TINGOUT=30 DP=10 -YGAPEXT=0.5	m Match 0% m Match 100% g first 45 sı	2000000000	satisfying	seqs,	##XX 6.00 .000	885 888	22, 2004,	
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163105 Breast C		Acad 1003 k1ce gene Acad 3729 Human foe Aaa62022 Hydrophob Aaa62032 Hydrophob Abk34832 Human cDN Aah14983 Human cDN Aah107167 Human rep Aal07168 Human rep Ab283399 Toxicolog Acd05761 cDNA enco Aaf94501 Human hyd Abt11190 Human sec	4673 Human 7153 Human 7565 Human 3995 CDNA 5077 CDNA 0270 Human 1456 Pseu 9516 Proka	Aas64820 DNA encod

ALIGNMENTS

RESULT 1
ABX92251
ID ABX92251
XX ABX92
XX ABX92
DT 08-M
XX Human
XX Human
XX Human
XX Homo
AX ABX92251 standard; cDNA; 365 BP. Human; gene; ss; ovarian specific nucleic acid; OSNA; ovarian cancer; non-cancerous ovarian disease; gene therapy; vaccine; cytostatic; gynaecological. 08-MAY-2003 (first entry) ABX92251; WPI; 2003-120677/11. P-PSDB; ABU61063. Salceda S, Macina RA, Sun Y, Liu C; 13-FEB-2001; 2001US-0268290P. 15-FEB-2001; 2001US-0268834P. 13-FEB-2002; 2002WO-US022271. Homo sapiens. Human ovarian specific nucleic acid DEX0310_65. (DIAD-) DIADEXUS INC. 21-NOV-2002. WO200292785-A2. Hu P, Recipon H, Karra K, Cafferkey R;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a new isolated nucleic acid termed ovarian CC specific nucleic acid (OSNA) comprising: (a) a nucleic acid molecule that CC encodes any of 53 fully defined protein sequences appearing as ABU61018-CC ABU61070 (termed ovarian specific proteins, OSP); (b) any of 76 fully CC defined nucleotide sequences appearing as ABU92187-ABX92262; or (c) a CC sequence having at least 60% sequence identity to the nucleic acid CC molecule of (a) or (b). Also included are a method for determining the presence of an ovary specific nucleic acid (OSNA) in a sample, a vector CC comprising an OSNA, a host cell comprising the vector, an isolated OSP CC polypeptide, an anti-OSP antibody or fragment, a method for determining CC the presence of an ovary specific protein in a sample and a vaccine CC comprising an OSP or OSNA. The methods and compositions of the present consprising an OSP or OSNA. The methods and compositions of the present conspination are useful for identifying, diagnosing, monitoring, staging, CC imaging and treating ovarian cancer and non-cancerous disease in ovary tissue. The present sequence is an OSNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated OSNA nucleic acid and encoded polypeptide, useful identifying, diagnosing, monitoring, staging, imaging and treat ovarian cancer and non-cancerous diseases in ovarian tissues.
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                              Arg 121
                                                                                                                                                       LeuGlyAgnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuLeuMetMet
                                                                                                                                                                                                      CAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCAT
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CGG 363
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Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide; antiarthritic; gene; ss.

WO200270539-A2

05-MAR-2002; 2002WO-US005095

05-MAR-2001; 2001US-00799451

(HYSE-) HYSEQ INC.

Tang YT Wehrman T, , Zhou P, Go Yang Y, Ma T, Wang J, Ma Y, Goodrich RW, Asundi V, Ma Y, Yamazaki V, Chen , Wang D, Drmanac RT; ø Zhang J, R, Wang Z, Zhao QA, Ghosh M; Ren Ę

P-PSDB; ABP68995. WPI; 2002-759812/82.

New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or por coagulation disorders.

Claim 1; SEQ ID NO 94; 1012pp + Sequence Listing; English.

The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ARZ11119-CARZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for cidentifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP6984) are useful as molecular weight comarkers, as a food supplement, for generating antibodies, in medical comarkers, as a food supplement, for generating antibodies, in medical comaring, screening and diagnostic assays and for treating cell-complificative discrete (cancer), neurodegenerative diseases (Parkinson's complificative discrete; neurodegenerative diseases (Parkinson's complification disorders, wound, burns, incision, ulcers, liver completes, lupus) genetic disorders, wound, burns, incision, ulcers, liver completes, infections (bacterial, viral, fungal, parasitic), complete fibrosis, infections (bacterial, viral, fungal, parasitic), complete fibrosis, infections (bacterial, viral, fungal, parasitic) continuing fibrosis, infections (bacterial, viral, fungal, parasitic) continuing fibrosis, infections (bacterial, viral, fungal, parasitic) continuing fibrosis, and for this patent did not form part continuing fibrosis, and for the printed specification, but was obtained in electronic format continuing fibrosis, and for the printed specification, but was obtained in electronic format continuing fibrosis and for the printed specification, but was obtained in electronic format continuing fibrosis and for the printed specification, but was obtained in electronic format continuing fibrosis and for the printed specification, but was obtained in electronic format continuing fibrosis and for the printed specification and format fibrosis and for the printed specification and format fibrosis and format fibrosis and for the printed specification and format fibrosis and for the printed specification and format fibrosis and format fibrosis

Sequence 562 BP; 95 A; 176 C; 174 G; 117 T; 0 U; 0 Other;

Percent Similarity:
Best Local Similarity:
Query Match:
DB: US-10-001-885-125 (1-121) x ABZ11212 (1-562) Alignment Scores: 146 ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGly 40 ATGGTGCGGATCTTGGCCAATGGGGAAAATCGTGCAGGACGACGACCCCCGAGTGAGGACC MetValArgI1eLeuAlaAsnGlyGluI1eValGlnAspAspAspProArgValArgThr 20 3.73e-51 632.00 100.00% 100.00% 100.00% Length: Matches: Conservative: Gaps: Mismatches: Indels: 562 0 0 0

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206 21

20-JAN-2003 (first entry)

RESULT 2
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ABZ11212

standard; cDNA; 562 BP

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11-APR-1997

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                                                                                                                                                                                                                                                                                                                                                                             06-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein gene 48 clone HFCAI74.
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97US-0040333P

97US-0040331P

97US-00403312P

97US-0043312P

97US-0043312P

97US-0043313P

97US-0043315P

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97US-0047581P 97US-0047583P 97US-0047583P 97US-0047584P 97US-0047586P 97US-0047586P 97US-0047588P 97US-0047589P 97US-0047599P 97US-0047593P 97US-0047594P 97US-0047594P 97US-0047594P 97US-0047599P 97US-0047599P

97US-0047503P

9703-0047600P 9703-0047601P 9703-0047613P 9703-0047613P 9703-0047613P 9703-0047613P 9703-0047633P 9703-0047633P 9703-0049610P 9703-005642P 9703-005663P 9703-0056631P 9703-0056631P 9703-0056631P 9703-0056631P 9703-0056631P 9703-0056631P 9703-0056631P 9703-0056845P 9703-0056845P 9703-0056845P 9703-0056881P 9703-0056881P 9703-0056884P 9703-0056894P 9703-0056894P 9703-0056894P 9703-0056894P 9703-0056894P 9703-0056894P 9703-0056894P 9703-0056894P 9703-0056894P 9703-0056994P 9703-0056994P 9703-0056994P 9703-0057650P 9703-0057650P

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a nucleic acid molecule designated Gene 48 from the human cDNA clone HFCAI74 (deposited as clone ATCC 97899 and ATCC 209045) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAVS9502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511- V99812; amino acid sequences AAV74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polymucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
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P-PSDB; AAW74778.
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                                                        GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis
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P, Young PE, G
en HS, Ebner R,
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RESULT 4

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97US-004031P,

97US-0043311P,

97US-0043313P,

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97US-0040334P.
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Вb Ş 밁 8 В 5 g 5

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Human, ss; gene; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn; nervous system disorders; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA #1 for novel secreted protein gene
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22-AUG-1997
23-AUG-1997
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97US-0056636P.
97US-0056663P.
97US-0056664P.
97US-0056845P.
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97US-0056862P.
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97US-0047633P.
97US-0048964P.
97US-004961P.
97US-004961P.
97US-0051926P.
97US-0055724P.
97US-0056630P.
                                                                                                                                                                                                                                                                       SCI INC.
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New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or
                                                                                                                                                                                                                             Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC;
Bedmarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, (
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebmer R,
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                              2002-634796/68
                                                                                                                                                                                                                                                                   Greene JM;
, Brewer LA;
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Example 1; SEQ ID ö 58; 129pp; English

preservative

RESULT 5
ACD82688
ID ACD8
XX
AC ACD8
XX
DT 22-S
XX
DE CDNA
XX

ACD82688 standard; cDNA; 1049 BP

22-SEP-2003 ACD82688;

(first entry)

cDNA sequence #48 containing

coding region of

ង

human secreted protein.

The invention relates to an isolated protein that is one of 186 human

Alignment Scores: disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional cencoding one of the novel human secreted proteins of the invention. Note: This sequence did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=6420526B1 secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification. The protein is used in a pharmaceutical composition used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders Sequence 1049 B₽; 223 A; 258 C; 303 G; 265 T; 0 U; 0 Other;

B &	Qy bb	φα VQ	D Qy	D Qy	од	Qy da	US-10-00	Pred. No.: Score: Score: Percent Si Best Local Buery Matcl DB:
121 Arg 121 	101 LeuGlyValArgGlyLeuLeuLeuValGlyLeuVal 	81 LeuGlyAsnHisAlaValG: 	61 GlnSerProPheAsnAspLe	41 AlaProProGlyGlyProG	21 ThrThrGlnProProArgGly	1 MetValArgIleLeuAlaA 116 ATGGTGCGGATCTTGGCCA	US-10-001-885-125 (1-121) x ABS73545	No.: 7.82e-51 632.00 1t Similarity: 100.00% 100.00% 100.00% 100.00% 100.00% 100.00% 6
	ouLeuValGlyLeuValTyr 	luProValThrSerIleLeu 	euAsnArgGlnLeuValAsn 	lyProArgGlnGlnGlnAla 	lySerIleProArgGlnSer 	euAlaAsnGlyGluIleValGlnAsp 	545 (1-1049)	Length: Matches: Conservative: Mismatches: Indels: Gaps:
	LeuGlyValArgGlyLeuLeuLeuValGlyLeuValTyrLeuValSerHisLeuSerGln 120	LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuLeuMetMet 100	GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis 80 	AlaProProGlyGlyProGlyProArgGlnGlnAlaGlyAlaArgLeuGlyAlaAla 60	ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGly 40	MetValargIleLeualaAsnGlyGluIleValGlnAspAspAspProArgValArgThr 20 		1049 121 0 0 0

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	Human; secreted prebreast cancer; wou haemophilia; thromal wiskott-Aldrich sy; graft-versus-host oviral infection; b renal disorder; kit angina pectoris; corespiratory disorder antiasthmatic; vir cerebroprotective; 970 07-MAR-1997; 970 07-MAR-1997; 970 07-MAR-1997; 970 07-MAR-1997; 970 11-APR-1997; 970 23-MAY-1997; 970 23-MAY-1	
97US-0047584P. 97US-0047584P. 97US-0047584P. 97US-0047588P. 97US-0047588P. 97US-004758PP. 97US-004759PP. 97US-0047592P. 97US-0047592P. 97US-0047593P. 97US-004759PP.	Human; secreted protein; hyperproliferative disorder; leukaemia; haemaphilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia; haemaphilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia; wiskott-Aldrich syndrome; autoimmune disorder; brook hymic hypoplasia; wiskott-Aldrich syndrome; autoimmune disorder; protein; viral hifection; host disease; Hashimoto's thyroiditis; allergy; asthma; viral hifection; host disease; Hashimoto's thyroiditis; allergy; asthma; viral hifection; host disease; finlaminoto's thyroiditis; allergy; asthma; recapitatory disease; kiney failure; cardiovascular disorder; cyrcostatic; respiratory disease; real disorder; expensive; antisathmatis; virucide; cardiovascular disorder; cyrcostatic; antisathmatis; virucide; fungicider; Alzheimer's disease; malkenmatis; virucide; fungicider; antisallergic; antianginal; carephroprotective; virucide; fungicide; antiallergic; antianginal; antiinflammatory; gene; ss. Homo sapiens. US2003049618-Al. 13-MAR-2001; 2001US-004033P. 07-MAR-1997; 97US-004016P. 07-MAR-1997; 97US-004331P. 11-APR-1997; 97US-00431P. 11-APR-1997; 97US-004356P. 11-APR-1997; 97US-0043	
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(RUBE/) RUBEN S (ROSE/) ROSEN SOPPET (CART/) CARTER (BEDN/) BENNARI (ENDR/) STUDRESS (YUGG/) YU G. (FENG/) FENG P. (YOUN/) YOUNG F (FERR/) FERRIE (DUAN/) DIAN D. (HUJJ/) HU J. (HUJJ/) HU J. (FILOR/) FICRENG (OLSE/) OLSEN H (FISC/) FISCHER (EENE/) EBNER F (EENE/) EBNER F	23-MAY-1997; 23-MAY-1998; 23-MAY-1998; 23-MAY-1998; 23-MAY-1998; 23-MAY-1998; 23-MAY-1997; 23-MAY-1998; 23-MAY-1997; 23-MAY-1998; 23-MAY-1997; 23-MAY-1998; 23-MAY-1997; 23-MA	
N S M. O C A. ET U C A. ER K C. ESS G A. ESS G A. D B. O D R. N D	97US-0047614P. 97US-0047611P. 97US-0047611P. 97US-0047611P. 97US-0047612P. 97US-004964P. 97US-0049610P. 97US-0049610P. 97US-0049610P. 97US-0056631P. 97US-0056631P. 97US-0056637P. 97US-0056637P. 97US-0056637P. 97US-0056684P. 97US-005687P. 97US-005687P. 97US-005687P. 97US-0056880P. 97US-0056881P. 97US-0056881P. 97US-0056881P. 97US-0056881P. 97US-0056881P. 97US-0056881P. 97US-0056889P. 97US-005689P. 97US-005699P. 97US-005699P. 97US-00569P.	

(ZENG/) (MOOR/) (SHIY/) (LAFL/) (LIYY/)) MOORE P A.
) SHI Y.
) LAFLEUR D W.
LI Y.
) ZENG Z.
) KYAW H.

Ruben SM, Rose Endress GA, Y Brewer Ę Rosen Moore PA, osen CA, Soppet DR, Carter KC, Bednarik DP, Yu G, Ni J, Feng P, Young PE, Greene JM, Fe J, Florence KA, Olsen HS, Fischer CL, Ebner Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, I Ferrie AM; Kyaw H;

WPI; 2003-521800/49. P-PSDB; ABO34421.

New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral

Claim 4; SEQ ID NO 58; 260pp; English.

CC disorders (e.g. lathendisconders (e.g. satth-versus-host disease, through automative disorders, host cells, antibodies, and recombinant methods considered producing human secreted proteins. The polypeptide and polynucleotide sequences for the secreted proteins are useful for preventing, treating, ambitorating or diagnosing medical conditions such as hyperproliferative disorders (e.g. leukaemia or breast cancers), wounds, reproductive conditions controlled the disorders, blood-related disorders (e.g. hasmophilia or thrombocytopaenia), immunodeficiencies (e.g. wiskott-Aldrich syndrome or thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease, controlled the sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma), controlled controlled the sclerosis or fingal infections (e.g. AIDS or sepsis), renal controlled controlled the schemal or congenital heart defects), respiratory confisorders (e.g. kidney failure), cardiovascular disorders (e.g. angina considers, neurological disorders (e.g. Alzheimer's disease). The polynucleotide or polypeptide may also be used as vaccine adjuvants. CC ACD82641-ACD82950 encode human secreted proteins or their fragments. CC ACD82641-ACD82950 encode human secreted proteins or their fragments. CC Note: The sequence data for this patent did not form part of the printed conspectification, but was obtained in electronic format directly from the conspection of the state of the printed conspectification, but was obtained in electronic format directly from the constant of the printed constants. and invention relates to the isolation of novel human secreted the polynucleotide sequences encoding them. The invention

Sequence 1049 BP; 223 A; 258 C; 303 G; 265 T; 0 U; 0 Other;

Best I Query DB: Percent Similarity: Best Local Similarity: US-10-001-885-125 (1-121) x ACD82688 No:: 7.82e-51 632.00 100.00% 100.00% 100.00% (1-1049)Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1049 121 0 0

8 片 Ś B Ś 밁 Ś 116 236 176 61 41 21 Н GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis AlaProProGlyGlyProGlyProArgGlnGlnGlnAlaGlyAlaArgLeuGlyAlaAla LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuLeuMetMet 100 CAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCAT ACTACCCAGCCAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAATAGGGGCCATGGT ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGly ATGGTGCGGATCTTGGCCAATGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACC MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspAspProArgValArgThr 355 80 295 60 235 40

> RESULT 6
> ABL90057
> ID ABL90
> ID ABL90
> ID ABL9
> ID Ś CC (ABB89040-ABB90441) useful for preventing, treating or ameliorating conditions e.g. by protein or gene therapy. The genes are consisted from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and covarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myccardial ischaemias; (d) wound healing (e) neurological disease e.g. cerebral anoxia and epilepsy; and (f) infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly c from WIPO at ftp.wipo.int/pub/published_pct_sequences 片 S 片 밁 The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative Homo Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antidicer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss. Claim Birse CE, 29-NOV-2001 Human polynucleotide SEQ ID NO 19-MAY-2000; 2000US-0205515P 18-MAY-2001; 2001WO-US016450. WO200190304-A2 ABL90057; 24-MAY-2002 ABL90057 2002-122018/16. sapiens. 476 121 416 356 4. 101 HUMAN GENOME ABB89648 Arg 121 standard; CGG 478 CTTGGTGTCGTGGCCTCCTGGTTGGCCTTGTCTACCTGGTGTCCCACCTGAGTCAG LeuGlyValArgGlyLeuLeuLeuValGlyLeuValTyrLeuValSerHisLeuSerGln 120 Rosen CA; ID NO 619; 2081pp + Sequence Listing; (first entry CDNA; 1108 뫈 619 English. 475 415

BP; 234

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324 ດ 271 H 0 u; 5

Other;

Alignment Scores: Pred. No.:

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Score:
Percent Similarity:
Best Local Similarity:
Query Match:
RESULT 7
ABN8980
ID ABN89
XX ABN89
XX ABN89
XX ABN89
XX Huma
XX Huma
XX Homc
XX Chrc
XX Homc
XX Homc
XX FPN WO20
XX 20-N
PR 27-N
PR 27-N
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PR 27-N
PR XX 10-N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ovary specific nucleic acid; OSNA; ovary specific protein; OSP; ovary specific gene; OSG; ovarian cancer; immune response; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ovary specific nucleic acid SEQ ID NO:31.
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                                                                    New ovary specific genes and proteins, useful as a vaccine for treating patients with ovarian cancer, or for diagnosing and monitoring the presence and metastases of ovarian cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200240535-A2.
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27-NOV-2000;
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                      Claim 1; Page 173-174; 260pp; English.
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Conservative:
Mismatches:
Indels:
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CC ABN87790 to ABN87882 represent human ovary specific nucleic acid (OSNA)
CC sequences, and ABB79297 to ABB79370 represent ovary specific protein
CC (OSP) sequences from the present invention. OSNA and OSP sequences have
CC cytostatic activity, and can be used in vaccine production and gene
CC therapy. An antibody that specifically binds to an OSP can be used for
CC treating a patient with ovarian cancer, particularly for inducing an
CC immune response against the ovarian cancer cell expressing the OSNA or
CC OSP. The OSNAs and OSPs can also be used for diagnosing and monitoring
CC the presence and metastases of ovarian cancer in a patient
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                Human breast tumour protein cDNA 15964.
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11-OCT-2000; 2000WO-US028255.
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99US-00417031

Harlocker SL, Dillon

Хu

2001-273773/28

New polypeptides encoded by polynucleotide sequences over-expressed breast tumor tissue are useful to detect, monitor and treat breast

Claim 13; Page 50; 52pp; English.

The present sequence encodes a breast tumour-associated protein. It was shown to have at least two-fold overexpression in breast tumour tissue. The invention relates to an isolated polypeptide comprising at least an immunogenic portion of a breast tumor-specific protein, or its variant that retains the ability to react with antigen-specific antisers. The breast tumour polynucleotides, polypeptides and antibodies are useful for inhibiting development of breast cancer. The polynucleotides may be used to design primers and probes for detecting and monitoring breast cancer

Sequence 550 BP; 102 A; 163 C; 164 G; 118 T; 0 U; 3 Other;

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                                                                                                             LeuGlyAsnHisAla-ValGluProValThrSerIleLeuLeuLeuPheLeuLeuMetMe
                                                                                                                                             CAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCAT
                                                                                                                                                                                                                                                                                             ATGGTGCGGATCTTGGCCAATGGGGAAATCGTGCAGGACGACGACCCCCGAGTGAGGACC
                                                                      tLeuGlyValArgGlyLeuLeuLeuValGlyLeuValTyrLeuValSerHisLeuSerGl
                                                                                                                                                                 GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis
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                                                                                              CTCGGCAACCATGCTTGTGGAGCCGGTGACCTCCATCCTGCT-CTCTTCCTGCTCATGAT
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Indels:
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31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                   30-MAR-2001; 2001WO-US008631.
                                                                                                                                   Homo sapiens.
                                                                                                                              WO200175067-A2
                                                                                               Drmanac RT,
                                                                                          2001-639362/73.
                                                                                                     HYSEQ
                                                                                               Liu C,
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

SEQ ID NO 624; 103pp; English.

The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCE) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbrrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in the constitution of genetic disorders or other that to assess biodiversity and the products of the treat of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 1165 BP; 247 A; 279 C; 342 G; 297 T; ď 0 Other,

Ov 1 Met Vallars	US-10-001-885-125 (1-121) x AAS64820 (1-1165)	DB:	Query Match:	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
rTleLenalaanGl	1) x AAS64820	v	68.67%	85.93%	86.67%	434.00	5.79e-32	
l WetValArgIleI.e);AlaAsnGlvCl);IleValGlnAsn-AsnAsnProArg	(1-1165)	Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:	
-AspAspProArc		ω	15	w	1	116	1165	

Ś 밁 S 맑 Ś 밁 472 412 352 40 20 83 GlyAlaAlaGln-SerProPheAsnAsp-LeuAsnArgGlnLeuVal-AsnMetGlyPhe CACTACCCAGCCACCAAGAGGTAGCATTCCTCGACAGAGCTTTCTTCAACAGGGGCCATG ThrThrGlnProProArgGlySerIleProArgGlnSer-PhePheAsnArgGlyHisG lyAlaProProGlyGlyPro-GlyProArgGlnGlnGlnAlaGly-----AlaArgLeu CAGCAAGCAGGCAAGGTGCCAAGGCTG gValArgTh 57 471 411 528 40 20

AAS64820
ID AAS6
XX AAS6
XX AAS6
XX DT 13-I
XX DE DNA
XX DE DNA
XX DE DNA
XX Huma
XX Huma
XX Huma

(first entry)

AAS64820 standard; cDNA; 1165 BP

DNA encoding 13-FEB-2002

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

novel human diagnostic protein #624.

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RESULT 10
ABX74673/c
ID 748774673/c
AC ABX7467
AC ABX74
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                                                      The present invention relates to a microarray comprising a matrix of at least one cDNA probe from a set of probes immobilised to a solid surface in a predetermined order, where a row of pixels corresponds to replicates of one distinct probe from the set. The probes are complementary to nucleic acid sequences that are expressed differentially in aggressive as compared to non-aggressive types of clear cell renal carcinoma (CC-RCC) and that hybridise to the probes under high stringency conditions. The microarray is useful for the propnosis of patients with CC-RCC, wherein aggressive and non-aggressive CC-RCC tumour types are characterised by differential expression profiles of genes that hybridise with one or more probes immobilised on the microarray. The arrays are useful for gene expression profiling of tumour and normal tissues. The present sequence represents a human CDNA sequence differentially expressed in aggressive vs. non-aggressive type CC-RCC phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New microarray, comprising a matrix of cDNA probe from a set of probes immobilized to a solid surface in predetermined order, useful in the prognosis of patients with clear cell renal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 459; 179pp; English.
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Sequence 1110

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11-DEC-2001; 2001US-0339453P.
14-MAR-2002; 2002US-0365091P.
14-MAR-2002; 2002US-0365394P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-0372615P.
22-APR-2002; 2002US-00128558.
24-APR-2002; 2002US-0376045P.
                                                                                      The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present DNA sequence represents a gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac F Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 219; 1177pp; English.
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P-PSDB; ADE08064.
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RESULT 12 ABS57565 Ś 밁 S 밁 S ঠ 밁 Ś 片 밁 Query Match: DB: US-10-001-885-125 Best Local Similarity: Baughn MR, Burford N, Din Gandhi AR, Gietzen KJ, Gr Lal PG, Lee EA, Lee S, L Swarnakar A, Ramkumar J, Warren BA, Yao MG, Xu Y, 30-MAR-2001; 2001US-0280527P.
06-APR-2001; 2001US-0282112P.
09-APR-2001; 2001US-0282702P.
13-APR-2001; 2001US-0283855P.
19-OCT-2001; 2001US-0343718P.
07-DEC-2001; 2001US-03457002P. hepatotropic; cytostatic; anti-HIV; antiallergic; antiasthmatic; cancer; antianaemic, antidabetic; antiinflammatory: neuroprotective; antiulcer; antirheumatic; antiarthritic; cardiant; hypotensive; gonadal dysgenesis; vasotropic; anticonvulsant; nootropic; immunosuppressive; pericarditis; antiparkinsonian; ophthalmological; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; angina pectoris; autoimmune disorder; AIDS; Crohn's disease; multiple sclerosis; epilepsy; ulcerative colitis; cardiovascular disorder; myocardial infarction; Raynaud's disease; myocarditis; neurological disorder; cataract; Expansud's disease; myocarditis; neurological disorder; cataract; huntington's disease; Myocarditis; neurological disorder; cataract; catara 29-MAR-2002; 2002WO-US009820 Homo Secreted protein; SECP; human; antiarteriosclerotic; antiatherosclerotic; Human SECP-21 cDNA from clone 1265837CD1 SEQ ID 11-FEB-2003 ABS57565; 10-OCT-2002 sapiens 424 -----TITGGTGAACTGAACAAAAACCTTATCAACATGGGCTTCACAAGGATGTATTTT 385 102 478 325 82 62 42 26 INCYTE GENOMICS INC. GGCCTGCAAGCCCTTGGACTAGTTGCTGTTCTTTGCCTTGTT GlyValArgGlyLeuLeuValGlyLeuValTyrLeuVal 115 GlyAsnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuLeuMetMetHeu SerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHisLeu GAGCCGGTTGGAGATGACTACAAG----CGCGGACAGCGGCCGAAGGAGAGCGAGCAGGATGTTGAAGACTCACAGAACCACACTGGT standard; GGAGAACGAATAGTGGAACCAGTAATAGTCATTTTCTTTTGGGTTATGCTGTGGTTCCTT ProproGlyGlyProGlyProArgGlnGlnAlaGlyAlaArgLeuGlyAlaAlaGln ArgGlySerIleProArgGlnSer------PhePheAsnArgGlyHisGlyAla (1-121) x ADE07153 (first 31.91% 17.48% entry , Ding L, Duggan BM, Elli J, Griffin JA, He A, Honc S, Lu DAM, Mason PM, Sar c J, Tang YT, Thangavelu K Ku Y, Yue H; ВP (1-1110) Mismatches: Indels: -----AAAATGGGAACACTT---Elliott VS, Honchell CD, , Sanjanwala M velu K, Tran U 21. Ęį. Forsythe Ison CH; Walia NK; ij 537 101 477 61 41 81 423

2003-058429/05.

Novel human secreted protein useful for treating, preventing or diagnosing cancer, hepatitis, psoriasis, asthma, diabetes mellitus, anemia, epilepsy, cataract, Alzheimer's disease.

Claim 101; Page 185-186; 188pp; English

CC antiarteriosclerotic, antiatherosclerotic, hepatotropic, cycostatic, antiateriosclerotic, antiatherosclerotic, antiatherosclerotic, antiatherosclerotic, antiathetic, antialaemic, antidiabetic, cartininflammatory, neuroprotective, antiulcer, antidiabetic, cantininflammatory, neuroprotective, antiulcer, antidiabetic, cantininflammatory, antiarthritic, cardiant, hypotensive, anticonvulsant, concerptor, immunosuppressive, antiparkinsonian and ophthalmological cativity. The polymucleotides and polypeptides of the invention can be cused for diagnosing, treating or preventing cell proliferative disorder c.g. arteriosclerosis, cirrhosis, hepatitis, cancer, cardiommune/inflammatory disorders e.g. acquired immunodeficiency syndrome c.g. altergies, asthma, anaemia, diabetes mellitus, Crohn's disease, cetc; cardiovascular disorder e.g. myocardial infarction, angina pectoris, competitus, carcer e.g. myocarditis, psoriasis, rheumatoid arthritis, cc hypertension, Raynaud's disease, myocardial infarction, angina pectoris, carcer, candiovascular disorders e.g. epilepsy, Huntington's disease, parkinson's disease, Alzheimer's disease, Creutzfeldt-Jakob disease, Parkinson's consenses, alzheimer's disease, Creutzfeldt-Jakob disease, Parkinson's consense in consense in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in cormal, carrier or affected individuals, and as hybridization probes for mapping naturally occurring genomic sequences. ABS5754-BBS57569

CC mapping naturally accurring genomic sequences. ABS5754-BBS97569

CC persesent cDNA's encoding the secreted proteins represented by ABB84649-CC ABB84673, described in the disclosure of the invention This invention describes novel secreted proteins (SECP) which have antiarteriosclerotic, antiatherosclerotic, hepatotropic, cytostatic,

Sequence 2999 BP; 912 A; 554 C; 585 ູດ 948 T; 0 U; 0 Other,

PheAsnArgGlyHisGlyAla	SerPhel	IleProArgGln	ArgGlySer	26	ફ
ArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGlyAla	SerPhel	IleproArgGln	ArgGlySer	26	Q
PheAsnArgGlyHisGlyAla	SerPhel	IleProArgGln	ArgGlySer	26	Ş
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ACA03995 standard; cDNA; 2668

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                                                                              US-10-001-885-125 (1-121) x ACA03995
                                                                                                                                   Percent Similarity:
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Query Match:
                                                                                                                                                                                                                                                                                            The invention relates to a combination comprising a plurality of cDNAs, or their complements that are differentially expressed in cancer and other proliferative disorders. The combination is useful in detecting changes in expression of genes encoding proteins that are associated with senescence and in diagnosing, staging, treating, or monitoring the progression or treatment of subjects with proliferative diseases such as cancer e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma; cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, colon, oesophagus, gall bladder, bone ganglia, heart, kidney, liver, lung, muscle, ovary, pancraas, parathyroid gland, penis, prostate, salivary glands, skin, small intestine, spleen, stomach, testis, thymus, thyroid and uterus. The present sequence represents cDNA of genes that are downregulated in senescent cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; senescence; ss; gene; cancer; proliferative disorder; leukaemia; adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma; adrenal gland cancer; bladder cancer; bone cancer; bone marrow cancer; brain cancer; breast cancer; cervical cancer; colon cancer; heart cancer; oesophageal cancer; gall bladder cancer; ganglial cancer; kidney cancer; liver cancer; lung cancer; muscle cancer; ovarian cancer; penile cancer; panctreatic cancer; parathyroid gland cancer; prostate cancer; salivary gland cancer; skin cancer; small intestine cancer; spleen cancer; stomach cancer; testicular cancer; thymic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New combination comprising cDNAs or their complements, useful for detecting changes in expression of genes encoding proteins associated with senescence, and in diagnosing, staging or treating proliferative diseases, e.g. cancer.
                                                                                                                                                                                                                                                               Sequence 2668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-328858/31.
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       Page 143-144; 195pp; English.
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HisAlaValGluProValThrSerIleLeuLeuLeuPheLeuLeuMetMetLeuGlyVal 103

The invention relates to novel isolated human secreted polypeptides (I) CC and polynucleotides (II). (I) and (II) are useful for treating conditions such as arthritis, nephritis. Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth can remodeling. (I) (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve can brain tissue and is useful for the treatment of central and correspond to the polypeptides. (I) are useful for the treatment of central and corresponding to the polypeptides. (I) are useful for the proliferation of neural cells and regeneration of nerve can brain such as Alzheimer's, parkinson's disease, Huntington's disease, and amyotrophic lateral corresponding to the proliferation of haematopolesis and is useful for treating mysloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers,

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19-MAY-2000; 2000US-00574454.

17-UUN-2000; 2000US-00596193.

14-JUL-2000; 2000US-00616847.

19-SEP-2000; 2000US-00665363.

20-OCT-2000; 2000US-00693267.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 158; 107pp; English.
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P-PSDB; AAU28177.
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders including severe combined immunodeficiency (SCID), bacterial c fungal infections, autroimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, in addition, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAS44920-AAS4595 represent novel human secreted protein coding sequences of the invention
                                                                                Human; prostate cancer; cytostatic; carcinogen; pharmacogenomic marker; gene; ss.
                                                                                                                                 Human prostate expression marker cDNA 30261
                 WO200160860-A2
                                                                                                                                                                                                     ABV30270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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16-MAR-2000; 2000US-0189862B.
25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
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CCCATCTCCCCCTTCACGCCGTCCACCCCGTCGATGCCACGCTTGCCCCTTCTCCCCTTG
                                                                                                                                    CCCTTTTCTCCTTTCAGTCCAAAGGCGCCGGGGTCTCCCTTGGGGGCCAGGGGGTCC----
                                                                                                                                                                                                  TCGTCTCCAGATGGTCCCGAGCTCCCCTGGTCTCCCCGCCTCAGCTCCAGGCTCG
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                                --HisLeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuLeuM
                                                                                                heAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrp----
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etMetLeuGlyValArgGlyLeuLeuLeu 108

3689 TAGCCCTTGGGTCCCCTGGAGCCCTTCTC 3717

Search completed: August 22, 2004, 08:37:48 Job time : 347 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

Database : -MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool_p/US10001885/runat_17082004_151718_25914/app_query.fasta_1.263
-Q=/cgn2 1/USPTO_spool_p/US10001885/runat_17082004_151718_25914/app_query.fasta_1.263
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bite -STRAFT=1 -EUD=-1 -MATRIX=blosum62 -TRAUS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10001885_@CGN 1 _5180 @prunat 17082004 _1S718N 25914 -NCPU=6 -ICPU=3
-NO MMAD -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Maximum Title: Perfect score: Command line parameters: Minimum Searched: Scoring table: Sequence: OM protein - nucleic search, using frame_plus_p2n model Total number of hits satisfying chosen parameters: Run on: DB seq length: 0
DB seq length: 2000000000 EST: * 27513289 segs, 14931090276 residues Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext BLOSUM62 US-10-001-885-125 632 August 22, 2004, 07:19:21; Search time 2464 Seconds (without alignments) MVRILANGEIVQDDDPRVRT......GVRGLLLVGLVYLVSHLSQR 121 em_estro:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS		484	BI522220	BE237465	CG607398	AA428101	BI414577	BY708262	BM714109	CG607245	BX523683	BCC85/5/	CF181245	CF363802	AK035688	AK008338	BU511854	BI905000	BF161467	BG862915	BI658578	CK129164	BB628297	CA527226	BU671222	AV591976	CB437353	##588875	DE054544	BE237464	AW462809	AA452397	BX420823	AW960624	BG331398	BE 904302	BY005712	BET 53.763	B1521387	CB296571	A942	ID
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REFERENCE	SOURCE ORGANISM	KEYWORDS	ACCESSION	DEFINITION	Locus	CA942977	RESULT 1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Frimates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 505)	Homo sapiens (human) Homo sapiens	EST.	mkNA sequence. CA942977	5 islet Homo sapiens cDNA clone IMA(CA942977 505 bp mRNA linear EST 30-DEC-2002		

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Percent Similarity:
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Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
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High quality sequence stop: 463.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: dmelton@biohp.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 617-495-1812
                                                                                                                                                      ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGly 40
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                                                                                                                                                                                                                                      ACTACCCAGCCACCAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAACAGGGGCCATGGT
                                                                                                                                                                                                                                                                                                                                     MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspAspAspProArgValArgThr
                                                                          CAGTCCCCCTTCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6607449"
/tissue_type="Purified pancreatic islet"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="HR85 islet"
/clone lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once Contact information: Hiroshi Incue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@ingate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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1 (bases 1 to 566)
1 (bases 1, Zollner, S., Enard, W., Ebersberger, I., Nickel, B. and
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12B22027_rev_1_B02_r_025.ab1 Chimpanzee brain library Koos Pan troglodytes CDNA clone 12B22027_rev_1_B02_r_025.ab1 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evolutionary Genetics
Max-Planck-Institute for evolutionary Anthropology
Deutscher Platz 6, 04103 Leipzig, Germany
Tel: +49-(0)-341-3550 550
Fax: +49-(0)-341-3550 555
Email: paabo@eva.mpg.de
Seq primer: M13 reverse.
                                                                                                                            1 MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspAspProArgValArgThr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Selection on human genes as revealed by comparisons to chimpanzee
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Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Pan troglodytes"
/mol_type="mRNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="brain, presumably cortex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
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21	hes:	2.99e-45 632.00 Y: 100.00% rity: 100.00%	t Scores:): Similarity: ;al Similarity:	Z O E . Z II
Tib="NIH_MGC 120" Tib="NIH_MGC 120" Torgan: pooled pancreas and spleen; Vector: Organ: pooled pancreas and spleen; Vector: PORT6; Site 1: Not1; Site 2: RORV (destroyed); RNA Anonymous pool of spleen and pancreas from 28 yo Library is oligo-dT primed and directionally cloned site is destroyed upon cloning). Average insert 5 kb, insert size range 1-2.5 kb. Library is 12ed and enriched for full-length clones and was 12ed and enriched for full-length clones and was 12ed by C. Gruber (Invitrogen). Research Genetics 12ed by C. Gruber (Invitrogen). Research Genetics 12ed code 025. Note: this is a NIH_MGC Library."	/clone_lib="NIH MGC 120" /clone_lib="NIH MGC 120" /note="Organ: pooled pancreas and spleen; /note="Organ: pooled pancreas and spectification of spleen and pancreas and pancreas and pancreas pooled by the primed and display to be specification of spleen and pancreas pooled by the primed and display to be specification of spleen and pancreas pooled by the primed and constructed by C. Gruber (Invitrogen). Reconstructed by C. Gruber (Invitrogen) and constructed by C. Gruber (Invitrogen) and pancreas pooled by C. Scholer (Invitrogen). The constructed by C. Gruber (Invitrogen) and pancreas pooled by C. Note: this is a NIH_MC tracking code 025. Note:	/clone_lib="NI /note="Organ: /note="Organ: pCMV-SPORT6; NS source anonymo male. Library (ECORV site; size 1.5 kb, i normalized and constructed by tracking code		ORIGIN
nsortium (LLNL) information can be	Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution informat found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11554 row: i column: 19 High qualify sequence stop: 688. Location/Qualifiers 1688 1688 1689 /organism="Homo sapiens" /mol type="mENNA" /db_xref="taxon:9606" /dlone="TMAGE:5220570" /lab host="mHOMO"	Tissue Procurement: Life Techno cDNA Library Preparation: Life cDNA Library Preparation: Life cDNA Library Preparation: Life cDNA Sequencing by: Incyte Geno Clone distribution: MGC clone found through the I.M.A.G.E. Co http://image.llnl.gov plate: LLAM11554 row: i colum High quality sequence stop: 688 1. 688 1. 688 /organism="Homo sapien /mol_type="maNNA" /db_xref="taxon:9606" /clone="IMAGE.5220570"	Tissu cDNA cDNA DNA Clon found found http: Plate High	FEATURES
ldae; Homo.	Primates; Catarrhini; Hom. nci.nih.gov/. of Health, Mammalian Gene ausberg, Ph.D.	Mammalia; Eutheria; Primates; C 1 (bases 1 to 688) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Unpublished (199) Contact: Robert Strausberg, Ph. Email: carphs-remail nih.gov	Mammalia; 1 (bases NIH-MGC ht National I Unpublishe Contact: R Email: Con-	REFERENCE AUTHORS TITLE JOURNAL COMMENT
linear EST 29-AUG-2001;lone IMAGE:5220570 5',	688 bp mRNA 0 Homo sapiens cDN 9	1 NIH_MGC nce. GI:1534 ns (human ns		RESULT 3 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
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uValSerHisLeuSerGln 120 :GGTGTCCCACCTGAGTCAG 528	eùGlyValArgGlyLeuLeuValGlyLeuValTyrLeuValSerHisLeuSerGln 	GlyValArgGlyLeuL GTGTTCGTGGCCTCC	101 Leu 469 CTT	אם אם
CCTCTTCCTGCTCATGATG 468	euGlyAsnHisAlaValGluProValThrSerIleLeuLeuPheLeuLeuPheLeuLeuMetMet 	GlyAsnHisAlaValG ggcAACCATGCTGTGG	81 Leu 409 CTG	dg VQ
RGGCTTTCCACAGTGGCAT 408	GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis 	SerProPheAsnAspL CCCCCTTCAATGACC	61 Gln 349 CAG	рb
TGCCAGGCTGGGTGCTGCT 348	GCTCCCCAGGGGGTCCTGGCCCCCGCCAGCAGCAGGAGGTGCCAGGCTGGGTGCTGCT	CCCCAGGGGGTCCTG	289 GCT	Db

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AUTHORS
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Homo sapiens
Rukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rukaryota, Metazoa; Chimates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 713)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
Chimatery Powersting ATCC
Chimatery Powersting ATCC
Chimatery Powersting ATCC
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BI193763.1 GI:14648783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1855 row: d column: 05 High quality sequence stop: 709.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/clome="IMAGE:5991412"
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/tissue_type="spithelioid carcinoma cell line"
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/lab host="MHOBE (phage-resistant)"
/clone lib="NHH MGC 42"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oligo-dT priming.
Site_3: EcoRI; cDNA made by oligo-dT priming.
Site_3: Sice_1: XhoI;
/site_3: Sice_1: XhoI;
/site_3: Sice_1: XhoI;
/site_3: Sice_3: 
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 714)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                  Email: cgapbs r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics,

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LICM1159 row: j column: 07

High quality sequence stop: 712.

Location/Qualifiers
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BF568253.1 GI:11641633
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602184629F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300518 5',
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'orqanism="Homo gapiens"
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Best Local Similarity:
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 765)
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Human UnigeneSet - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
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                                                                                                                                                                                                                                                                                                                          BX095713 Soares total fetus ND2HF8 9w Homo sapiens CDNA clone INAGD998B081942 ; IMAGE:787879, mRNA sequence.

EX095713
                                                                                                                                                                                                                                                                                                BX095713.1 GI:27842493
                                                                                                                                                                                                                                      Homo sapiens (human)
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/tissue_type="epithelioid carcinoma cell line"
/lab host="DH108 (phage-resistant)"
/clone lib="NIH MGC_42"
/clone lib="NIH MGC_42"
/clone lib="NIH MGC_42"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCAGCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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US-10-001-885-125 (1-121) x BX095713 (1-765)
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RZPDLIB; I.M.A.G.E.'CDNA Clone Collection;
Human UnigeneSet - RZPDJ (RZPDLIB NO.972)

http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany

"Tel: +49 30 32639 101

Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. M13r, Primer sequence: TTCACACAGGAAACAGCTATGAC.
                                                                                                                                       CAGTCCCCTTCAATGACCTCAACCGGCAGCTGGTGAACATGGGCTTTCCGCAGTGGCAT
                                                                                                                                                                                                  GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis
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                                                                                  LeuGlyValArgGlyLeuLeuLeuValGlyLeuValTyrLeuVal8erHisLeuSerGln 120
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 CGG 407
                         Arg 121
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/dev_stage="8-9 weeks"
/lab_host="DH10B"
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|mol_type="mRNA"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM9689 row: n column: 17
High quality sequence stop: 711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 980)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                       AlaProProGlyGlyProGlyProArgGlnGlnAlaGlyAlaArgLeuGlyAlaAla
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BG331398
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Contact: Robert Strausberg, Ph.D.

Email: Ggapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLCM1244 row: j column: 17

High quality sequence stop: 636.

Location/Qualifiers
272
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1 (bases 1 to 1104)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                           AlaProProGlyGlyProGlyProArgGlnGlnGlnAlaGlyAlaArgLeuGlyAlaAla 60
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/tlssue_type="large_cell_carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_18"
/clone_lib="NIH_MGC_
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/db_xref="taxon:9606"
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Hegde P., Qi.R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
Assessment of gene expression patterns in a model of colon to
metastasis using a 19,200 element cDNA microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 3528
Fax: 301 838 0208
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Plate: 148
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                                                                                          CCACCAAGAGGTAGCATTCCTCGACAGAGCTTCTTCAACAGGGGCCATGGTGCTCCCCCA
                                                                                                                     ProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGlyAlaProPro 43
                                                                                                                                                                                    ATCTTGGCCAATGGGGAAATCGTGCAGGATGACGACCCCCGAGTGAGGACCACTACCCAG
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/mol type="mXNA"
/db_xref="taxon:9606"
/clone lib="WAGE resequences, |
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